

\*\*\*\*\*  
WQ5REH  
(TM)  
\*\*\*\*\*

Release 3.1A John F. Collins, BioComputing Research Unit.  
Copyright (C) 1993-1998 University of Edinburgh, U.K.  
Distribution rights by Oxford Molecular Ltd

MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Mar 7 21:10:00 2000; MasPar time 3.88 Seconds  
122.160 Million cell updates/sec

Tubular output not generated.

Title: >US-08-981-824-1  
Description: (1-20) from US08981824.ppe  
Perfect Score: 146  
Sequence: 1 DVNYAFHLATDLPACDGER 20

Scoring table: PAM 150  
Gap 15

Searched: 188963 seqs, 23586106 residues

Post-processing: Minimum Match 08.  
Listing first 45 summaries

Database: f:geneseq35  
i:geneseqp

Statistics: Mean=20.820; Variance 63.757; scale 0.327

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES			
Result No.	Score	Query Match Length DB ID	Description Pred. No.
1	146	100.0	20 1 W01793 Human 65 kD glutamine 4.60e-09
2	146	100.0	20 1 W18842 65 kD Glutamic acid de 4.60e-09
3	146	100.0	503 1 R23645 Human GAD65 gene produ 4.60e-09
4	146	100.0	540 1 R59520 GAD65 1-45 N-terminal- 4.60e-09
5	146	100.0	544 1 R59524 GAD65 545-585 C-termin 4.60e-09
6	146	100.0	534 1 R59518 GAD65 1-31 deleted, C 4.60e-09
7	146	100.0	584 1 W86017 Human GAD65 protein se 4.60e-09
8	146	100.0	584 1 W34519 Human GAD65 protein. 4.60e-09
9	146	100.0	585 1 W12402 65 kD human glutamic a 4.60e-09
10	146	100.0	585 1 W14915 Modified glutamic acid 4.60e-09
11	146	100.0	585 1 R28756 Human pancreatic islet 4.60e-09
12	146	100.0	585 1 R59516 Human GAD65. 4.60e-09
13	146	100.0	585 1 R79105 Human glutamic acid de 4.60e-09
14	146	100.0	585 1 W14916 Modified glutamic acid 4.60e-09
15	146	100.0	585 1 R71641 Human GAD. 4.60e-09
16	146	100.0	585 1 R29629 Human GAD 65. 4.60e-09
17	146	100.0	585 1 W35361 Human 65K-glutamic aci 4.60e-09
18	135	92.5	585 1 R23644 Rat GAD65 gene product 1.07e-07
19	135	92.5	585 1 R29628 Rat GAD 65. 1.07e-07
20	135	92.5	605 1 R71733 Rat glutamic acid deca 1.07e-07
21	129	88.4	584 1 W86018 Rat GAD65 protein sequ 5.88e-07
22	129	88.4	584 1 W34520 Rat GAD65 protein. 5.88e-07
23	128	87.7	540 1 R59521 GAD65 1-45 N-terminal- 7.80e-07

24	128	87.7	544	1	R59525	GAD65 545-585 C-termin	7.80e-07
25	128	87.7	554	1	R59519	GAD65 1-31 deleted, C4	7.80e-07
26	128	87.7	585	1	R59517	Rat GAD65.	7.80e-07
27	99	67.8	14	1	R75649	Peptide derived from h	2.38e-03
28	99	67.8	14	1	W18857	65 kD Glutamic acid de	2.38e-03
29	93	63.7	20	1	R72267	Glutamic acid decarbox	1.19e-02
30	85	58.2	20	1	R72266	Glutamic acid decarbox	9.85e-02
31	63	43.2	533	1	R37585	E.coli malate synthase	2.49e+01
32	61	41.8	593	1	R27220	Brain GAD #2.	4.01e+01
33	61	41.8	594	1	R27221	Full length brain GAD.	4.01e+01
34	61	41.8	594	1	R74716	Amino acid sequence of	4.01e+01
35	61	41.8	594	1	R74717	Amino acid sequence of	4.01e+01
36	61	41.8	594	1	R27222	Full length islet GAD.	4.01e+01
37	61	41.8	666	1	W31268	Mouse frizzled-3 prote	4.01e+01
38	58	39.7	190	1	R98922	Murine APPL1 (aa21-210	8.12e+01
39	58	39.7	273	1	W82006	Human adult brain secr	8.12e+01
40	58	39.7	343	1	R97222	Human G-protein couple	8.12e+01
41	58	39.7	424	1	R63441	Trichoderma harzianum	8.12e+01
42	58	39.7	653	1	R98903	Murine APPL1.	8.12e+01
43	58	39.7	663	1	R40923	Alcohol oxidase.	8.12e+01
44	57	39.0	848	1	R80551	Human Ah receptor prot	1.02e+02
45	57	39.0	2707	1	W27161	Mouse receptor ME2.	1.02e+02

ALIGNMENTS

RESULT 1  
ID W01793 standard; peptide; 20 AA.  
AC W01793;  
DT 15-OCT-1997 (first entry)  
DE Human 65 kD glutamine decarboxylase peptide.  
KW Human; glutamine decarboxylase; GAD; diagnosis; predisposition;  
KW tumour; immunological; disease; autoimmune; diabetes; reagent;  
KW determination; T cell; subpopulation; medication; treatment;  
KW prevention; production; antigen; immunogen; tolerogen; isolation;  
KW reinjection; inactivation.  
OS Homo sapiens.  
PN DE19525784-A1.  
PD 16-JAN-1997.  
PF 14-JUL-1995; 025784.  
PR 14-JUL-1995; DE-025784.  
PA (BOEF) BOEHRINGER MANNHEIM GMBH.  
PI Albert W. Boitard C. Endl J. Jung G. Schendel D;  
PI Stahl P. Van Endert P;  
DR WPI: 97-078452/08.  
PT Glutamine decarboxylase peptide(s) - for diagnosis and therapy of diabetes, etc.  
PS Claim 1; Page 12; 15pp; German.  
CC The present peptide is a fragment of the human 65 kD glutamine decarboxylase (GAD), which can be used to diagnose, or diagnose a predisposition to, a tumour or immunological disease, preferably an autoimmune disease, especially diabetes. It can also be used as a reagent to determine specific T cell subpopulations, in medicaments to treat or prevent immunological diseases, preferably autoimmune diseases, especially diabetes, to produce antigens, especially immunogens or tolerogens and to isolate specific T cell subpopulations, which can be used to produce antigens or for reinjection, optionally after inactivation.  
SQ Sequence 20 AA;

Query Match 100.0%; Score 146; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 4.60e-09;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 DVNYAFHLATDLPACDGER 20  
QY 1 DVNYAFHLATDLPACDGER 20

RESULT 2  
ID W18842 standard; peptide; 20 AA.  
AC W18842;  
DT 05-JAN-1998 (first entry)



Query Match 100.0%; Score 146; DB 1; Length 544;  
Best Local Similarity 100.0%; Pred. No. 4.60e-09;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 86 DVNYAFELHATDLPACDGER 105  
QY 1 DVNYAFELHATDLPACDGER 20

RESULT 6  
ID R59518 standard; protein; 554 AA.  
AC R59518;  
DT 09-NOV-1994 (first entry)  
DE GAD65 1-31 deleted, C45A mutant.  
KW GAD65; glutamate-decarboxylase; diabetes mellitus;  
KW stiff man syndrome; autoantibody; mutagenesis.  
OS Homo sapiens.  
PN WO9412529-A.  
PD 09-JUN-1994.  
PF 02-DEC-1993; U11705.  
PR 03-DEC-1992; US-984935.  
PA (REGC ) UNIV CALIFORNIA.  
PI Baekkeskov S, Kim J, Namchuk M, Richter W, Shi Y;  
DR WPI; 94-200193/24.  
DT New soluble fragments of glutamic acid decarboxylase protein -  
PT used for the diagnosis and treatment of insulin dependent  
PT diabetes mellitus and stiff man syndrome.  
PS Disclosure; Fig. 1; 73pp; English.  
CC The amino acid sequences of human GAD65 (R59516) and rat GAD65  
CC (R59517) were determined. New soluble fragments of GAD65  
CC (R59518-25) were prepared by deletion/substitution  
CC mutagenesis. These fragments are free of N-terminal amino acids  
CC that limit solubility. Different fragments contain epitopes for  
CC different classes of GAD65 autoantibodies.  
SQ Sequence 554 AA;

Query Match 100.0%; Score 146; DB 1; Length 554;  
Best Local Similarity 100.0%; Pred. No. 4.60e-09;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 55 DVNYAFELHATDLPACDGER 74  
QY 1 DVNYAFELHATDLPACDGER 20

RESULT 7  
ID W86017 standard; protein; 584 AA.  
AC W86017;  
DT 22-FEB-1999 (first entry)  
DE Human GAD65 protein sequence.  
KW GAD65; autoantibody; soluble; detection; diagnosis; monitor; IDDM;  
KW insulin-dependent diabetes mellitus; stiff man syndrome.  
OS Homo sapiens.  
PN US849506-A.  
PD 15-DEC-1998.  
PF 25-MAY-1995; 450755.  
PR 02-DEC-1993; US-161290.  
PR 03-DEC-1992; US-984935.  
PR 25-MAY-1995; US-450755.  
PA (REGC ) UNIV CALIFORNIA.  
PI Baekkeskov S, Kim J, Namchuk M, Richter W, Shi Y;  
DR WPI; 99-069720/06.  
DT Immunoassay for GAD65 auto-antibodies - used for diagnosis of  
PT diabetes and stiff man syndrome  
PS Examples; Fig 1; 31pp; English.  
CC This represents a human GAD65 protein sequence. The invention provides  
CC soluble fragments of GAD65 that are specifically reactive with at least  
CC one class of GAD65 autoantibody. The fragments are substantially free of  
CC N-terminal amino acids that would otherwise limit solubility. Different  
CC fragments contain different epitopes for different classes of GAD65  
CC autoantibodies. These fragments are used in the methods of the invention  
CC for detection of GAD65 autoantibodies. The methods are used for  
CC diagnosing or monitoring insulin-dependent diabetes mellitus (IDDM) and

CC stiff man syndrome.  
SQ Sequence 584 AA;

Query Match 100.0%; Score 146; DB 1; Length 584;  
Best Local Similarity 100.0%; Pred. No. 4.60e-09;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 86 DVNYAFELHATDLPACDGER 105  
QY 1 DVNYAFELHATDLPACDGER 20

RESULT 8  
ID W34519 standard; protein; 584 AA.  
AC W34519;  
DT 24-MAR-1998 (first entry)  
DE Human GAD65 protein.  
KW GAD65; glutamic acid decarboxylase protein; human; soluble fragment;  
KW autoantibody; insulin-dependent diabetes mellitus; IDDM; diagnosis;  
KW stiff man syndrome; therapy.  
OS Homo sapiens.  
PN US5891448-A.  
PD 23-NOV-1997.  
PF 02-DEC-1993; 161290.  
PR 02-DEC-1993; US-161290.  
PR 03-DEC-1992; US-984935.  
PA (BAEK/) BAEKESKOV S.  
PA (KIMJ/) KIM J.  
PA (NAMC/) NAMCHUK M.  
PA (RICH/) RICHTER W.  
PA (SHIY/) SHI Y.  
PI Baekkeskov S, Kim J, Namchuk M, Richter W, Shi Y;  
DR WPI; 98-017711/02.  
DT Soluble fragments of glutamic acid decarboxylase GAD65 - used to  
PT distinguish between insulin-dependent diabetes mellitus and  
PT stiff-man syndrome  
PS Disclosure; column 27-30; 30pp; English.  
CC This sequence represents the human glutamic acid decarboxylase protein  
CC GAD65. The invention relates to soluble fragments of a GAD65 protein that  
CC are specifically reactive with a GAD65 autoantibody (AAB), where the  
CC fragment is at least 99% pure and the AAB binds to a conformational  
CC epitope of the fragment. The soluble GAD65 fragments can be used to  
CC distinguish between insulin-dependent diabetes mellitus (IDDM) and stiff  
CC man syndrome. They can also be used for diagnosis and treatment of IDDM  
CC and stiff man syndrome. The fragments can distinguish different temporal  
CC stages in the progression of IDDM.  
SQ Sequence 584 AA;

Query Match 100.0%; Score 146; DB 1; Length 584;  
Best Local Similarity 100.0%; Pred. No. 4.60e-09;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 86 DVNYAFELHATDLPACDGER 105  
QY 1 DVNYAFELHATDLPACDGER 20

RESULT 9  
ID W12402 standard; protein; 585 AA.  
AC W12402;  
DT 08-OCT-1997 (first entry)  
DE 65 kD human glutamic acid decarboxylase isoform.  
KW 65 kD glutamic acid decarboxylase; human; GAD65; enzyme; pancreas;  
KW neuron; central nervous system; type I diabetes; autoimmune response;  
KW T cell; therapy.  
OS Homo sapiens.  
PN WO9700891-A1.  
PD 09-JAN-1997.  
PF 24-JUN-1996; U10790.  
PF 23-JUN-1995; US-494624.  
PA (KENN-) KENNEDY INST RHEUMATOLOGY.  
PA (NEUR-) NEUROCRINE BIOSCIENCES INC.  
PA (SBAR-) ST BARTHOLOMEW'S HOSPITAL CENT CLINICAL.

PI Conlon PJ, Gaur A, Leslie RDG, Ling N, Londei M;  
 DR WPI: 97-087322/08.  
 DR N-PSDB; T61097.  
 PT New human glutamic acid decarboxylase peptide(s) - used for  
 PT treatment, diagnosis and determining predisposition to diabetes and  
 PT for ameliorating auto-immune responses.  
 PS Disclosure: Fig 1: 28pp; English.  
 CC This sequence represents the 65 kD isoform of human glutamic acid  
 CC decarboxylase (GAD65). GAD is an enzyme expressed in the beta cells of  
 CC the pancreas, and in neurons of the central nervous system. There are two  
 CC isoforms of GAD, a 67 kD isoform, and GAD65. Immunodominant regions of  
 CC GAD65 have been identified in Type I diabetic patients. Fragments of  
 CC GAD65, and analogues of the fragments, are used in the methods of the  
 CC invention. The methods are for detecting or treating diabetes or a  
 CC predisposition to diabetes. The peptides can also be used for  
 CC ameliorating an autoimmune response in a patient. Alteration of the  
 CC native peptides with selective changes of crucial residues can induce  
 CC unresponsiveness or change the responsiveness of antigen-specific  
 CC autoreactive T cells. The peptide analogues compete for binding to MHC  
 CC and do not cause proliferation of the corresponding native  
 CC peptide-specific T cells.  
 SQ Sequence 585 AA;

Query Match 100.0%; Score 146; DB 1; Length 585;  
 Best Local Similarity 100.0%; Pred. No. 4.60e-09;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 86 DVNYAFHLHATDLLPACDGER 105  
 QY 1 DVNYAFHLHATDLLPACDGER 20  
 |||||

RESULT 10  
 ID W14915 standard; Protein; 585 AA.  
 AC W14915;  
 DT 10-JUL-1997 (first entry)  
 DE Modified glutamic acid decarboxylase (K396R).  
 KW Glutamic acid decarboxylase; GAD; autoimmune disease; therapy;  
 KW insulin-dependent diabetes mellitus; vaccine;  
 KW enzyme engineering; protein engineering.  
 OS Synthetic.  
 PN W09712034-A1.  
 PD 03-APR-1997.  
 PF 27-SEP-1996; SE1210.  
 PR 29-SEP-1995; SE-003379.  
 PA (SYNE-) SYNETICS BIOTECHNOLOGY AB.  
 PI Essen-Moeller A, Falorni A, Lernmark A, Robertson J;  
 DR WPI: 97-212895/19.  
 DR N-PSDB; T64560.  
 PT Modified glutamic acid decarboxylase for autoimmune disease  
 PT treatment - has immunoreactivity of unmodified GAD65 but decreased  
 PT enzyme activity, esp. useful for insulin-dependent diabetes mellitus  
 PT treatment  
 PS Claim 3: Page 13-15; 24pp; English.  
 CC A modified human glutamic acid decarboxylase (GAD) (W14915) has the  
 CC native lysine residue at amino acid position 396 replaced by  
 CC arginine. It is obtd. by site-directed mutagenesis (see also  
 CC T64561) of native human GAD65 cDNA and expression of the mutant DNA  
 CC (T64560) in transformed host cells. Lys-396 is critical for enzyme  
 CC activity. By replacing it with an amino acid incapable of Schiff  
 CC base formation, immunoreactivity is maintained but enzyme activity  
 CC is reduced or lost, so minimising the risk of toxicity. The  
 CC modified GAD can be used to treat and/or prevent autoimmune  
 CC disorders such as insulin-dependent diabetes mellitus (IDDM) and  
 CC other diseases, e.g. neurological diseases, esp. in individuals  
 CC having a genetic predisposition for IDDM or with an increased  
 CC antibody titre against GAD.  
 SQ Sequence 585 AA;

Query Match 100.0%; Score 146; DB 1; Length 585;  
 Best Local Similarity 100.0%; Pred. No. 4.60e-09;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 86 DVNYAFHLHATDLLPACDGER 105  
 QY 1 DVNYAFHLHATDLLPACDGER 20  
 |||||

RESULT 11  
 ID R28756 standard; Protein; 585 AA.  
 AC R28756;  
 DT 20-APR-1993 (first entry)  
 DE Human pancreatic islet cell glutamic acid decarboxylase.  
 KW GAD; insulin dependent diabetes melting; IDDM; autoantibody detection.  
 OS Homo sapiens.  
 PN W09220811-A.  
 PD 26-NOV-1992.  
 PF 14-MAY-1992; U04079.  
 PR 15-MAY-1991; US-702162.  
 PA (UNIW ) UNIV WASHINGTON.  
 PA (ZYMO ) ZYMOGENETICS INC.  
 PI Foster DC, Grubin CE, Hagopian W, Karlisen AE, Lernmark A, Ohara PJ;  
 DR WPI: 92-415789/50.  
 DR N-PSDB; Q31783.  
 PT Polynucleotide encoding human islet glutamic acid decarboxylase -  
 PT used to test for auto-antibodies against itself to diagnose  
 PT insulin dependent diabetes mellitus  
 PS Disclosure; Fig 2: 45pp; English.  
 CC The sequence is that of human pancreatic islet glutamic acid  
 CC decarboxylase (GAD) which is used to test biological samples for  
 CC the presence of autoantibodies to human GAD. It can also be used  
 CC to remove antibodies against GAD from plasma in order to treat an  
 CC autoimmune response to GAD, e.g. in insulin-dependent diabetes  
 CC (IDDM), and may also be used to induce immunological tolerance to GAD  
 CC by giving GAD that specifically binds the GAD receptor on immature T  
 CC or B cells.  
 SQ Sequence 585 AA;

Query Match 100.0%; Score 146; DB 1; Length 585;  
 Best Local Similarity 100.0%; Pred. No. 4.60e-09;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 86 DVNYAFHLHATDLLPACDGER 105  
 QY 1 DVNYAFHLHATDLLPACDGER 20  
 |||||

RESULT 12  
 ID R59516 standard; protein; 585 AA.  
 AC R59516;  
 DT 09-NOV-1994 (first entry)  
 DE Human GAD65.  
 KW GAD65; glutamate-decarboxylase; diabetes mellitus;  
 KW stiff man syndrome; autoantibody.  
 OS Homo sapiens.  
 PN W09412529-A.  
 PD 09-JUN-1994.  
 PF 02-DEC-1993; U11705.  
 PR 03-DEC-1992; US-984935.  
 PA (REGC ) UNIV CALIFORNIA.  
 PI Baekkeskov S, Kim J, Namchuk M, Richter W, Shi Y;  
 DR WPI: 94-200193/24.  
 PT New soluble fragments of glutamic acid decarboxylase protein -  
 PT used for the diagnosis and treatment of insulin dependent  
 PT diabetes mellitus and stiff man syndrome.  
 PS Disclosure; Fig. 1; 73pp; English.  
 CC The amino acid sequences of human GAD65 (R59516) and rat GAD65  
 CC (R59517) were determined. New soluble fragments of GAD65  
 CC (R59518-25) were prepared by deletion/substitution  
 CC mutagenesis. These fragments are free of N-terminal amino acids  
 CC that limit solubility. Different fragments contain epitopes for  
 CC different classes of GAD65 autoantibodies.  
 SQ Sequence 585 AA;

Query Match 100.0%; Score 146; DB 1; Length 585;  
 Best Local Similarity 100.0%; Pred. No. 4.60e-09;



Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 86 DVNYAFELHATDLLPACDGER 105  
 QY 1 DVNYAFELHATDLLPACDGER 20

RESULT 13

ID R79105 standard; Protein: 585 AA.  
 AC R79105;  
 DT 13-NOV-1995 (first entry)  
 DE Human glutamic acid decarboxylase (GAD65).  
 KW Rat glutamic acid decarboxylase; GAD65; autoimmune disorders;  
 KW insulin-dependent diabetes mellitus; stiff man disease.  
 OS Homo sapiens.  
 PN W09507992-A.  
 PD 23-MAR-1995.  
 PF 24-AUG-1994; U09478.  
 PR 17-SEP-1993; US-123859.  
 PA (REGC ) UNIV CALIFORNIA.  
 PI Clare-Selzler MJ, Erlander MG, Kaufman DL, Tobin AJ;  
 DR WPI; 95-131360/17.  
 DR N-PSDB; Q86482.  
 PT New polypeptide fragments of glutamic acid decarboxylase - for  
 PT diagnosis and treatment of autoimmune disease, esp. insulin  
 PT dependent diabetes, also related nucleic acid, vectors,  
 PT antibodies, hybridoma(s) etc.  
 PS Example 1; Fig 3; 100pp; English.  
 CC Q86481 and Q86482 encode R71733 and R79105, rat and human glutamic  
 CC acid decarboxylase (GAD65) respectively, from which the GAD65  
 CC fragments described in R72261-R72298 were derived. These fragments  
 CC can be used to detect autoantibodies against GAD, e.g. to diagnose  
 CC and treat GAD-related autoimmune disorders, such as insulin  
 CC dependent diabetes mellitus or stiff man disease.  
 SQ Sequence 585 AA;

Query Match 100.0%; Score 146; DB 1; Length 585;  
 Best Local Similarity 100.0%; Pred. No. 4.60e-09;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 86 DVNYAFELHATDLLPACDGER 105  
 QY 1 DVNYAFELHATDLLPACDGER 20

RESULT 14

ID W14916 standard; Protein: 585 AA.  
 AC W14916;  
 DT 10-JUL-1997 (first entry)  
 DE Modified glutamic acid decarboxylase.  
 KW Glutamic acid decarboxylase; GAD; autoimmune disease; therapy;  
 KW insulin-dependent diabetes mellitus; vaccine;  
 KW enzyme engineering; protein engineering.  
 OS Synthetic.  
 FH Key  
 FT misc\_difference 396  
 FT W09712034-A1.  
 PN 03-APR-1997.  
 PD 27-SEP-1996; SE1210.  
 PR 29-SEP-1995; SE-003379.  
 PA (SYNE-) SYNECTICS BIOTECHNOLOGY AB.  
 PI Essen-Moeller A, Falorni A, Lernmark A, Robertsson J;  
 DR WPI; 97-212895/19.  
 PT Modified glutamic acid decarboxylase for autoimmune disease  
 PT treatment - has immunoreactivity of unmodified GAD65 but decreased  
 PT enzyme activity, esp. useful for insulin-dependent diabetes mellitus  
 PT treatment  
 PS Claim 1; Page 16-18; 24pp; English.  
 CC A modified human glutamic acid decarboxylase (GAD) (W14915) has the  
 CC native lys residue at amino acid position 396 replaced by Ile, Gln,  
 CC His, Gly or esp. Arg (see also W14915). It is obtd by site-  
 CC directed mutagenesis of native human GAD65 cDNA and expression of

CC the mutant DNA in transformed host cells. Lys-396 is critical for  
 CC enzyme activity. By replacing it with an amino acid incapable of  
 CC Schiff base formation, immunoreactivity is maintained but enzyme  
 CC activity is reduced or lost, so minimising the risk of toxicity.  
 CC The modified GAD can be used to treat and/or prevent autoimmune  
 CC disorders such as insulin-dependent diabetes mellitus (IDDM) and  
 CC other diseases, e.g. neurological diseases, esp. in individuals  
 CC having a genetic predisposition for IDDM or with an increased  
 CC antibody titre against GAD.  
 SQ Sequence 585 AA;

Query Match 100.0%; Score 146; DB 1; Length 585;  
 Best Local Similarity 100.0%; Pred. No. 4.60e-09;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 86 DVNYAFELHATDLLPACDGER 105  
 QY 1 DVNYAFELHATDLLPACDGER 20

RESULT 15

ID R71641 standard; Protein: 585 AA.  
 AC R71641;  
 DT 21-SEP-1995 (first entry)  
 DE Human GAD.  
 KW GAD; glutamic-acid-decarboxylase; glutamate-decarboxylase;  
 KW non-insulin-dependent diabetes; NIDDM; diagnosis; autoantibody;  
 KW pancreas; islet.  
 OS Homo sapiens.  
 FH Key  
 FT binding\_site 394..399  
 FT /label= Pyridoxal-5'-phosphate\_binding\_site  
 PN W09507464-A.  
 PD 16-MAR-1995.  
 PF 02-SEP-1994; U09937.  
 PR 07-SEP-1993; US-117907.  
 PA (UNIW ) UNIV WASHINGTON.  
 PI Hagopian W, Karlisen AE, Landin-Olsson M, Lernmark A;  
 DR WPI; 95-123512/16.  
 DR N-PSDB; Q86046.  
 PT Predicting the clinical course of diabetes in patients with  
 PT non-insulin dependent diabetes mellitus - by detecting the  
 PT presence of auto-antibodies to human islet cell glutamic acid  
 PT decarboxylase.  
 PS Claim 8; Page 40-44; 62pp; English.  
 CC A human islet cDNA library was screened for colonies containing  
 CC GAD cDNA using probes (given in Q86047-49) based on conserved  
 CC internal and N- and C-terminal regions of cat, rat and mouse brain  
 CC GAD. Full-length clones were obtained by PCR-RACE. The entire  
 CC sequence of the human islet GAD cDNA is given in Q86046 and the  
 CC encoded protein in R71641. GAD was used to screen sera for the  
 CC presence of GAD autoantibodies.  
 SQ Sequence 585 AA;

Query Match 100.0%; Score 146; DB 1; Length 585;  
 Best Local Similarity 100.0%; Pred. No. 4.60e-09;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 86 DVNYAFELHATDLLPACDGER 105  
 QY 1 DVNYAFELHATDLLPACDGER 20

Search completed: Tue Mar 7 21:10:07 2000  
 Job time : 7 secs.

**THIS PAGE BLANK (USPTO)**

**THIS PAGE BLANK (USPTO)**



```

REFERENCE #A1935
#authors Bu, D.F.; Erlander, M.G.; Hitz, B.C.; Tillaekaratne, N.J.K.;
          Kautman, D.L.; Wagner-McPherson, C.B.; Evans, G.A.; Tobin,
          A.J.
#journal Proc. Natl. Acad. Sci. U.S.A. (1992) 89:2115-2119
#title Two human glutamate decarboxylases, 65-kDa GAD and 67-kDa
#cross-references GAD, are each encoded by a single gene.
#accession M01D:92196068
#molecule_type mRNA
#residues 1-585 #label BU1
#cross-references GB:M81882; NID:g182933; PIDN:AAA62367.1; PID:g182934
#experimental_source brain
#note #sequence extracted from NCBI backbone (NCBI:88007)
REFERENCE #A1292
#authors Karlisen, A.E.; Hagopian, W.A.; Grubin, C.E.; Dube, S.;
          Distcheche, C.M.; Adler, D.A.; Baermeier, H.; Mathewes, S.;
          Gratt, F.J.; Foster, D.; Lernermark, A.
#journal Proc. Natl. Acad. Sci. U.S.A. (1991) 88:8337-8341
#title Cloning and primary structure of a human islet isoform of
#cross-references glutamic acid decarboxylase from chromosome 10.
#accession A1292
#molecule_type mRNA
#residues 1-585 #label KAR
#cross-references GB:M74826; NID:g182931; PIDN:AAA58491.1; PID:g182932
#experimental_source pancreatic islet
REFERENCE #S30058
#authors Mauch, L.; Abney, C.C.; Berg, H.; Scherbaum, W.A.; Liedvogel,
          B.; Northmann, W.
#journal Eur. J. Biochem. (1993) 212:597-603
#title Characterization of a linear epitope within the human
#cross-references pancreatic 64-kDa glutamic acid decarboxylase and its
#cross-references autoimmune recognition by sera from insulin-dependent
#cross-references diabetes mellitus patients.
#accession S30058
#molecule_type mRNA
#residues 6-585 #label MAU
#cross-references EMBL:X69936
#experimental_source pancreatic islet
REFERENCE #A54778
#authors Bu, D.F.; Tobin, A.J.
#journal Genomics (1994) 21:222-228
#title The exon-intron organization of the genes (GAD1 and GAD2)
#cross-references encoding two human glutamate decarboxylases (GAD-67 and
#cross-references GAD-65) suggests that they derive from a common ancestral
#cross-references GAD.
#cross-references M01D:94375018
#contents annotation; intron-exon boundaries
COMMENT This enzyme (GAD) catalyzes the formation of an inhibitory
          neurotransmitter, gamma-aminobutyric acid, from L-glutamic acid;
          it has several isoforms, each encoded by a separate gene. GAD has
          also been implicated as an autoantigen in autoimmune disease
          stiff-man syndrome and insulin-dependent diabetes mellitus.
GENETICS GDB:GAD2
#gene #cross-references GDB:128595; OMIM:138275
#map_position 10p11.23-10p11.23
CLASSIFICATION #superfamily human glutamate decarboxylase
KEYWORDS carbon-carbon lyase; carboxy-lyase; phosphoprotein; pyridoxal
          phosphate
FEATURE 396 #binding_site pyridoxal phosphate (lys) (covalent)
          #status predicted
SUMMARY #length 585 #molecular-weight 65411 #checksum 4799
Query Match 100.0%; Score 146; DB 1; Length 585;
Best Local Similarity 100.0%; Pred. No. 1,56e-19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 86 DYNVAFLLHATDILLPACDGER 105
|||||

```

---

```

QY 1 DYNVAFLLHATDILLPACDGER 20
RESULT 3
ENTRY JC4064 #type complete
TITLE glutamate decarboxylase (EC 4.1.1.15) 65k chain - pig
ORGANISM #formal_name Sus scrofa domestica #common_name domestic pig
DATE 30-Jun-1995 #sequence_revision 14-Jul-1995 #text_change
ACCESSIONS JC4064
REFERENCE JC4064
#authors Suzuki, R.; Asami, N.; Amann, E.; Wagatsuma, M.
#journal Gene (1995) 152:257-260
#title Sequences of two porcine glutamic acid decarboxylases (65- and
#cross-references 67-kDa GAD).
#accession JC4064
#molecule_type mRNA
#residues 1-585 #label SUZ
#cross-references DDBJ:D31848; NID:g790964; PIDN:BAH06635.1;
#experimental_source brain
#note #sequence extracted from NCBI backbone (NCBI:88007)
COMMENT This enzyme catalyzes the conversion of glutamic acid into
          gamma-aminobutyric acid.
CLASSIFICATION #superfamily human glutamate decarboxylase
KEYWORDS carbon-carbon lyase; carboxy-lyase
FEATURE 393-396 #domain DOPA decarboxylase binding #status predicted
          #label BIN
SUMMARY #length 585 #molecular-weight 65388 #checksum 5933
Query Match 99.3%; Score 145; DB 2; Length 585;
Best Local Similarity 95.0%; Pred. No. 2,81e-19;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
DB 86 EYNYAFLLHATDILLPACDGER 105
|||||
QY 1 DYNVAFLLHATDILLPACDGER 20
RESULT 4
ENTRY JH0423 #type complete
TITLE glutamate decarboxylase (EC 4.1.1.15) 2 - rat
ALTERNATE_NAMES glutamate decarboxylase GAD65; L-glutamate 1-carboxy-lyase
ORGANISM #formal_name Rattus norvegicus #common_name Norway rat
DATE 31-Mar-1992 #sequence_revision 23-Mar-1995 #text_change
ACCESSIONS JH0423
REFERENCE JH0423
#authors Erlander, M.G.; Tillaekaratne, N.J.K.; Feldblum, S.; Patel,
          N.; Tobin, A.J.
#journal Neuron (1991) 7:91-100
#title Two genes encode distinct glutamate decarboxylases.
#cross-references M01D:91299343
#accession JH0423
#molecule_type mRNA
#residues 1-585 #label ERL
#cross-references GB:M72422; NID:g204225; PIDN:AAA63488.1; PID:g204226
#experimental_source brain
#note the authors translated the codon GAT for residue 86 as
          HIs, TCA for residue 198 as Ala, and CAG for residue
          428 as Trp
REFERENCE A60888
#authors Chang, Y.C.; Gottlieb, D.I.
#journal J. Neurosci. (1988) 8:2123-2130
#title Characterization of the proteins purified with monoclonal
#cross-references antibodies to glutamic acid decarboxylase.
#accession A60888
#molecule_type preliminary
#status preliminary
#residues 'V',191-194, 'X',196-203, 'XX',206-219, 'X',225-234, 'X',
          236-247, 'X',249-266, 'X',524-537,539-543, 'V',547-549,

```

	COMMENT	This enzyme (GAD) catalyzes the formation of an inhibitory neurotransmitter, gamma-aminobutyric acid, from L-glutamic acid; it has several isoforms, each encoded by a separate gene.
	CLASSIFICATION	#superfamily human glutamate decarboxylase
	KEYWORDS	carbon-carbon lyase; carboxy-lyase; phosphoprotein; pyridoxal phosphate
FEATURE	396	#binding_site pyridoxal phosphate (Lys) (covalent)
SUMMARY		#status predicted #length 585 #molecular-weight 65402 #checksum 7756
Query Match	92.5%; Score 135; DB 1; Length 585;	
Best Local Similarity	Pred. NO. 9.76e-17;	
Matches	18; Conservative 2; Mismatches 0; Indels 0; Gaps 0;	
Db	86 DVMYALHATDLPACDGER 105	:     :     :
Qy	1 DVNYAFHLMTDLPLPACDGER 20	
RESULT	5	B36182 #type complete
ENTRY		protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type
TITLE		PRP69D precursor - fruit fly ( <i>Drosophila melanogaster</i> )
ALTERNATE_NAMES		protein-tyrosine-phosphatase DPTP
ORGANISM		#formal_name <i>Drosophila melanogaster</i>
DATE		10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
ACCESSIONS		B36182
REFERENCES		A36182
Authors		Streuli, M.; Krueger, N.X.; Tsai, A.Y.M.; Saito, H.
#journal		Proc. Natl. Acad. Sci. U.S.A. (1989) 86:8698-8702
#title		A family of receptor-linked protein tyrosine phosphatases in humans and <i>Drosophila</i> .
#cross-references	MUID:90046860	
#accession	B36182	
#status		preliminary; not compared with conceptual translation
#molecule_type	mRNA	
#residues	1-1462 #label STR	
#cross-references	GB:M27699; NID:g158188; PIDN:AAZ28842.1; PID:g158189	
GENETICS		
#gene	Ptgp69D	
#cross-references	FBN0014007	
CLASSIFICATION		#superfamily protein-tyrosine-phosphatase, receptor type
	PRP69D; fibronectin type III repeat homology;	
	immunoglobulin homology; leukocyte common antigen cytosolic domain homology; protein-tyrosine-phosphatase homology	
glycoprotein; phosphoprotein; phosphoric monoester hydrolase; transmembrane protein; tyrosine-specific phosphatase		
KEYWORDS		
FEATURE		
1-28		#domain signal sequence #status predicted #label SIG\
29-1462		#product protein-tyrosine-phosphatase, receptor type
	PRP69D #status Predicted #label MAT\	
29-806		#domain extracellular #status predicted #label EXT\
38-114		#domain immunoglobulin homology #label IMI\
147-216		#domain immunoglobulin homology #label IM2\
807-823		#domain transmembrane #status predicted #label TMN\
824-1462		#domain intracellular #status predicted #label INT\
917-1145		#domain protein-tyrosine-phosphatase homology #label PTP\
1213-1439		#domain protein-tyrosine-phosphatase homology #label PRP2\
45-112,154-214		#disulfide bonds #status predicted
1097		#active-site Cys (phosphocysteine intermediate) #status predicted
1103		#binding_site substrate phosphate (Arg) #status predicted
1391		#active-site Cys (phosphocysteine intermediate) #status predicted
1397		#binding_site substrate phosphate (Arg) #status predicted
SUMMARY		#length 1462 #molecular-weight 167410 #checksum 8905

Query Match	45.2%; Score 65; DB 1; Length 1462;	
Best Local Similarity	35.0%; Pred. No. 4.97e-01;	
Matches	7; Conservative 7; Mismatches 6; Indels 0; Gaps 0;	
Db	888 DDYGFLEYEMPNRFSR 907	: : : :~ : : :
Qy	1 DVNYAFHLMTDLPLPACDGER 20	
RESULT	6	B44509 #type complete
ENTRY		aldose 1-epimerase (EC 5.1.3.3) - <i>Streptococcus thermophilus</i>
TITLE		#formal_name <i>Streptococcus thermophilus</i>
ORGANISM		10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
ACCESSIONS		B44509
REFERENCE		B44509
Authors		Poolman, B.; Royer, T.J.; Mainzer, S.E.; Schmidt, B.F.
#journal		J. Bacteriol. (1990) 172:4037-4047
#title		Carbohydrate utilization in <i>Streptococcus thermophilus</i> : characterization of the genes for aldose 1-epimerase (mutarotase) and UDPglucose 4-epimerase.
#cross-references	MUID:90299833	
#accession	B44509	
#status		preliminary
#molecule_type	DNA	
#residues	1-348 #label POO	
#cross-references	EMBL:M38175; NID:g153748; PID:g153750	
CLASSIFICATION		#superfamily aldose 1-epimerase
KEYWORDS		isomerase
SUMMARY		#length 348 #molecular-weight 39012 #checksum 5351
Query Match	43.8%; Score 64; DB 1; Length 348;	
Best Local Similarity	57.1%; Pred. No. 1.18e+00;	
Matches	8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;	
Db	221 ETWYDFRTDILP 234	:   :
Qy	1 DVNYAFHLMTDILP 14	
RESULT	7	DWECL #type complete
ENTRY		L-serine dehydratase (EC 4.2.1.13) 1 - <i>Escherichia coli</i>
TITLE		L-serine deaminase 1
ALTERNATE_NAMES		#formal_name <i>Escherichia coli</i>
ORGANISM		30-Jun-1991 #sequence_revision 21-Nov-1997 #text_change 18-Jun-1999
DATE		
ACCESSIONS		F64942; JVO036
REFERENCE		A64720
Authors		Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Colado-Vides, J.; Glasner, J.D.; Rode, C.K.; Mayhew, G.F.; Gregor, J.; Davis, N.W.; Kirkpatrick, H.A.; Goeden, M.A.; Rose, D.J.; Mau, B.; Shao, Y.
#journal		Science (1997) 277:1453-1462
#title		The complete genome sequence of <i>Escherichia coli</i> K-12.
#cross-references	MUID:97426617	
#accession	F64942	
#status		preliminary; nucleic acid sequence not shown; translation not shown
#molecule_type	DNA	
#residues	1-454 #label BLAT	
#cross-references	GB:AEO0275; GB:U00096; NID:g1788106; PID:AACT4884.1; PID:g1788116; UWGP:d1814	
REFERENCE		JVO036
Authors		Su, H.; Lang, B.F.; Newman, E.B.
#journal		J. Bacteriol. (1989) 171:5095-5102
#title		L-serine degradation in <i>Escherichia coli</i> K-12: cloning and sequencing of the sdaA gene.
#cross-references	MUID:89359152	

```

#accession: JY0036
##molecule-type DNA
##residues 7-219,'N',221-454 ##label SUH
##cross-references GB:M2893
##experimental-source strain K12
COMMENT This enzyme converts L-serine to pyruvate.
GENETICS
#gene sda
CLASSIFICATION #superfamily microbial L-serine dehydratase
KEYWORDS carbon-oxygen lyase; gluconeogenesis; hydro-lyase; lyase;
pyridoxal phosphate; serine catabolism
SUMMARY #length 454 #molecular-weight 48906 #checksum 2174

Query Match 43.8% Score 64; DB 1; Length 454;
Best Local Similarity 50.0%; Pred. No. 1.18e+00;
Matches 8; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Db 167 VPYFKSATLHAYCN 182
1 1 1 1 1 1 1 1 1 1
QY 2 VNYAFHLHATDLPACD 17

RESULT 8
ENTRY #type complete
TITLE nudel protein precursor - fruit fly (Drosophila melanogaster)
ORGANISM #forma_name Drosophila melanogaster
DATE 27-Oct-1995 #sequence_revision 27-Oct-1995 #text_change
16-Jul-1999
ACCESSIONS A57096
REFERENCE A57096
#authors Hong, C.C.; Hashimoto, C.
#journal Cell (1995) 82:785-794
#title An unusual mosaic protein with a protease domain, encoded by
the nudel gene, is involved in defining embryonic
dorsoventral polarity in Drosophila.
#cross-references MIMD:95401268
#accession A57096
##status preliminary; not compared with conceptual translation
##molecule-type mRNA
##residues 1-2616 ##label HON
#cross-references GB:U29153; NID:g984320; PID:g984321
GENETICS
#gene FlyBase:nd1
##cross-references FlyBase:FBgn0002926
CLASSIFICATION #superfamily LDL receptor ligand-binding repeat homology;
trypsin homology
KEYWORDS extracellular protein
FEATURE
891-929 #domain LDL receptor ligand-binding repeat homology
#label LDL1\
1145-1378 #domain trypsin homology #label TRY\
1396-1430 #domain LDL receptor ligand-binding repeat homology
#label LDL7\
1776-1811 #domain LDL receptor ligand-binding repeat homology
#label LDL12\
2310-2344 #domain LDL receptor ligand-binding repeat homology
#label LDL8\
2421-2457 #domain LDL receptor ligand-binding repeat homology
#label LDL3
SUMMARY #length 2616 #molecular-weight 292372 #checksum 9962

Query Match 43.8% Score 64; DB 2; Length 2616;
Best Local Similarity 47.1%; Pred. No. 1.18e+00;
Matches 8; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Db 2390 FTYIQTADPSKICDKR 2406
:::|||||
QY 4 YAFHLHATDLPACDGR 20

RESULT 9
ENTRY #type complete
TITLE Killer toxin KP4 precursor - Usutuago maydis virus P4

```

```

ORGANISM      #formal_name Ustilago maydis virus P4, Univ-P4
DATE          19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change
              13-Sep-1998
ACCESSIONS    S40034; S14734
REFERENCE      #authors      Park, C.M.; Byenn, J.A.; Ganesa, C.; Flurkey, W.F.; Bozarth, R.F.; Koltin, Y.
#journal      Mol. Microbiol. (1994) 11:155-164
#title        Structure and heterologous expression of the Ustilago maydis
              viral toxin KP4.
#cross-references M01D:94195103
#accession     S40034
##molecule_type mRNA
##residues     1-127 ##label PAR
REFERENCE      ##cross-references EMBL:L12226
S14734
#authors      Ganesa, C.; Flurkey, W.H.; Randhawa, Z.I.; Bozarth, R.F.
#journal      Arch. Biochem. Biophys. (1991) 286:195-200
#title        Ustilago maydis virus P4 killer toxin: characterization,
              partial amino terminus sequence, and evidence for
              glycosylation.
#cross-references M01D:91378288
#accession     S14734
##molecule_type Protein
##residues     23-52 ##label GAN
KEYWORDS       toxin
FEATURE        #domain signal sequence #status predicted #label SIG
1-22           #product killer toxin KP4 #status experimental #label
1-22           MAT
23-127         #length 127 #molecular-weight 13489 #checksum 9326
SUMMARY        #length 127 #molecular-weight 13489 #checksum 9326
Query Match    43.2%; Score 63; DB 2; Length 127;
Best Local Similarity 50.0%; Pired. No. 1,80e+00;
Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
Db 5 NWVSYFLFAAMLP 18
      :|::|||::||
OY 1 DVNYAFLLHATDLP 14
RESULT 10
ENTRY
TITLE      SYECMA #type complete
ORGANISM   malate synthase (EC 4.1.3.2) A - Escherichia coli
DATE       #formal_name Escherichia coli
          31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change
          18-Jun-1999
ACCESSIONS A33649; A30378; E65208; Q00592
REFERENCE   S05692
#authors    Byrne, C.
#submission submitted to the EMBL Data Library, July 1988
#accession  A33649
##molecule_type DNA
##residues 1-533 ##label BYR1
REFERENCE   A30378
#authors    Byrne, C.R.; Stokes, H.W.; Ward, K.A.
#journal    Nucleic Acids Res. (1988) 16:10924
#title      Nucleotide sequence of the aceB gene encoding malate synthase
              A in Escherichia coli.
#cross-references M01D:89083515
#accession  A30378
##molecule_type DNA
##residues 1-533 ##label BYR2
REFERENCE   A64720
#authors    Blatter, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.;
              Burland, V.; Riley, M.; Collado-Vides, J.; Glasner, J.D.;
              Rode, C.K.; Mayhew, G.F.; Gregor, J.; Davis, N.W.;
              Kirpatrick, H.A.; Goeden, M.A.; Rose, D.J.; Mau, B.; Shao,
              Y.
              Science (1997) 277:1453-1462
#title      The complete genome sequence of Escherichia coli K-12.
#cross-references M01D:97426617
#accession  E65208

```

```
##status      preliminary: nucleic acid sequence not shown;
##molecule_type DNA
##residues    1-533 #label BLAT
##cross-references GB:AE000474; GB:U00096; NID:91790440;
                PID:91790444; PID:91790444; UMG:bd4014
##experimental_source strain K-12, substrain MG1655
GENETICS
#gene         acbB
#map_position 91 min
CLASSIFICATION #superfamily malate synthase
KEYWORDS      carbon-carbon lyase: glyoxylate bypass: oxo-acid-lyase
SUMMARY       #length 533 #molecular-weight 60273 #checksum 1098

Query Match      43.2%; Score 63; DB 1; Length 533;
Best Local Similarity 66.7%; Pred. No. 1.80e+00;
Matches          8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db      402 ADOLAPDGER 413
QY      9 ATDLPLACDGER 20

RESULT  11
ENTRY   A72009 #type complete
TITLE   fumarate hydratase Chlamydia pneumoniae (strain CWL029)
ORGANISM #formal_name Chlamydia pneumoniae
DATE     23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change
                22-Jun-1999
ACCESSIONS A72009
REFERENCE   A72000
#authors    Kaiman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.;
            Ollinger, L.; Grimwood, J.; Davis, R.W.; Stephens, R.S.
#journal     Nature Genet. (1999) 21:385-389
#title       Comparative genomes of Chlamydia pneumoniae and C.
            trachomatis.
#cross-references MIMD:99206606
#accession   A72009
#status      preliminary
#molecule_type DNA
#residues    1-460 #label ARN
#cross-references GB:AE001681; GB:AE001363; NID:94377330;
                PIDN:AD9150.1; PID:94377343
##experimental_source strain CWL029
GENETICS
#gene         func
CLASSIFICATION #superfamily fumarate hydratase
SUMMARY       #length 460 #molecular-weight 50441 #checksum 6630

Query Match      42.5%; Score 62; DB 2; Length 460;
Best Local Similarity 46.2%; Pred. No. 2.74e+00;
Matches          6; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Db      362 IIFYNLOSVDLS 374
QY      2 VNYAFLHATDLP 14

RESULT  12
ENTRY   S66947 #type complete
TITLE     hypothetical protein YOR064c - yeast (Saccharomyces
            cerevisiae)
ALTERNATE_NAMES #hypothetical protein O2815
ORANISM        #formal_name Saccharomyces cerevisiae
DATE           12-Jul-1996 #sequence_revision 12-Jul-1996 #text_change
                14-Nov-1997
ACCESSIONS    S66947
REFERENCE     S66929
#authors      Bohn, C.; Bolotin-Fukuhara, M.; Daignan-Fornier, B.; Dang,
            D.V.; Valens, M.
#submission   Submitted to the Protein Sequence Database, July 1996
#accession    S66947
#molecule_type DNA

##residues    1-219 #label BOH
##cross-references EMBL:Z74972; NID:91420208; PID:e251980; PID:91420209;
                MIPS:YOR064c
##experimental_source strain 5288C
GENETICS
#map_position 15R
SUMMARY       #length 219 #molecular-weight 25350 #checksum 6074

Query Match      41.8%; Score 61; DB 2; Length 219;
Best Local Similarity 47.1%; Pred. No. 4.16e+00;
Matches          8; Conservative 4; Mismatches 4; Indels 1; Gaps 1;

Db      12 DIRSFSTIDHP-CE 27
QY      1 DVNYAFLHATDLPACD 17

RESULT  13
ENTRY   I59173 #type complete
TITLE   glutamate decarboxylase - rat
ORGANISM #formal_name Rattus norvegicus #common_name Norway rat
DATE     02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
                22-Jun-1999
ACCESSIONS I59173
REFERENCE   I59173
#authors    Bond, R.W.; Wyborski, R.J.; Gottlieb, D.I.
            Proc. Natl. Acad. Sci. U.S.A. (1990) 87:8771-8775
#journal     Developmentally regulated expression of an exon containing a
            stop codon in the gene for glutamic acid decarboxylase.
#cross-references MIMD:91062362
#accession   I59173
#status      preliminary: translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues    1-223 #label RES
#cross-references GB:M8350; NID:9204231; PIDN:AA41185.1; PID:9204232
CLASSIFICATION #superfamily human glutamate decarboxylase
SUMMARY       #length 223 #molecular-weight 25069 #checksum 1388

Query Match      41.8%; Score 61; DB 2; Length 223;
Best Local Similarity 47.4%; Pred. No. 4.16e+00;
Matches          9; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Db      91 ETDFSNLFADDLPAKNGE 109
QY      1 DVNYAFLHATDLPACDGE 19

RESULT  14
ENTRY   S49897 #type complete
TITLE     hypothetical narbonin-like 2S protein (clone pVFNA4) - fava
            bean
ORGANISM        #formal_name Vicia faba #common_name fava bean
DATE           05-Mar-1995 #sequence_revision 14-Jul-1995 #text_change
                26-Aug-1999
ACCESSIONS    S49897
REFERENCE     S49848
#authors      Nong, V.; Schlessier, B.; Muentz, K.
#submission   Submitted to the EMBL Data Library, November 1994
#description   The narbonin gene from Vicia faba L.
#accession    S49897
#status      preliminary
#molecule_type mRNA
#residues    1-286 #label NON
#cross-references EMBL:Z46834; NID:9600103; PID:9600104
##experimental_source seed
CLASSIFICATION #superfamily alcohol sulfotransferase
KEYWORDS      seed; storage protein
SUMMARY       #length 286 #molecular-weight 32575 #checksum 1900

Query Match      41.8%; Score 61; DB 2; Length 286;
Best Local Similarity 31.3%; Pred. No. 4.16e+00;
Matches          5; Conservative 6; Mismatches 5; Indels 0; Gaps 0;
```

```
Db      129 DINEYIKSDELFVNC 144
      1:|:|:::|:|
QY      1 DVNYAFLLHATDLLPAC 16
```

RESULT	15
ENTRY	

```
ENTRY      S49848      #type complete
TITLE      probable narbonin - jack bean
ORGANISM   #formal_name Canavalia ensiformis #common_name jack bean
DATE       06-Mar-1995 #sequence_revision 12-May-1995 #text_change
           26-Aug-1999
```

ACCESSIONS	S49848
REFERENCE	S49848

**authors** Nong, V.; Schlesier, B.; Muentz, K.  
**#submission** Submitted to the EMBL Data Library, November 1994  
**#description** A cDNA encoding putative narboxin from *Canavalia ensiformis*.  
**#accession** S49848  
**#molecule** cDNA

Query Match	41.8%;	Score 61;	DB 2;	Length 287;
Best Local Similarity	31.3%;	Pred. NO. 4.16e+00;		
Matches	5;	Conservative	6;	Mismatches 5;
				Indels 0;
				Gaps 0;

```
Db      129 DINYEYIKSDELFVNC 144
        1:11::: :1: 1
QY      1 DVNYAFLHATDLLPAC 16
```

Search completed: Tue Mar 7 21:07:51 2000  
Job time : 9 secs.



\*\*\*\*\*  
MUSE  
\*\*\*\*\*  
(TW)

Release 3.1A John F. Collins, Biocomputing Research Unit.  
Copyright (c) 1993-1998 University of Edinburgh, U.K.  
Distribution rights by Oxford Molecular Ltd

Msrch\_p protein - protein database search, using Smith-Waterman algorithm  
Run on: Tue Mar 7 21:02:37 2000; MasPar time 3.45 Seconds  
Tabular output not generated. 173.144 Million cell updates/sec

Title: >US-08-981-824-1  
Description: (1-20) from US08981824.dep  
Perfect Score: 146  
Sequence: 1 DVNVAFLNATDLPACDGER 20

Scoring table: PAM 150  
Gap 15

Searched: 82229 seqs, 29866866 residues

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: swiss-prot38  
1:swissprot

Statistics: Mean 29.144; Variance 36.336; scale 0.802

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	146	100.0	585	1 DCE2_HUMAN	GLUTAMATE DECARBOXYLASE	7.49e-22
2	146	100.0	585	1 DCE2_MOUSE	GLUTAMATE DECARBOXYLASE	7.49e-22
3	145	99.3	585	1 DCE2_PIG	GLUTAMATE DECARBOXYLASE	1.44e-21
4	135	92.5	585	1 DCE2_RAT	GLUTAMATE DECARBOXYLASE	8.98e-19
5	66	45.2	1462	1 PTP6_DROME	PROTEIN-TYROSINE PHOSPHATASE	1.46e-01
6	64	43.8	454	1 GALM_STRTR	ALDOSE 1-EPIMERASE (EC 3.72e-01)	3.72e-01
7	64	43.8	454	1 SDHL_ECOLI	L-SERINE DEHYDRATASE (EC 3.72e-01)	3.72e-01
8	64	43.8	2616	1 NDL_DROME	SERINE PROTEINASE	5.90e-01
9	63	43.2	127	1 KP4T_UNIV4	KP4 KILLER TOXIN PRECURSOR	5.90e-01
10	63	43.2	396	1 YNAG_RHISN	HYPOTHETICAL 42.8 KD P	5.90e-01
11	63	43.2	533	1 MASY_ECOLI	MALATE SYNTHASE A (EC 5.90e-01)	5.90e-01
12	61	41.8	593	1 DCE1_MOUSE	GLUTAMATE DECARBOXYLASE	1.46e+00
13	61	41.8	593	1 DCE1_RAT	GLUTAMATE DECARBOXYLASE	1.46e+00
14	61	41.8	594	1 DCE1_PIG	GLUTAMATE DECARBOXYLASE	1.46e+00
15	61	41.8	594	1 DCE1_FELCA	GLUTAMATE DECARBOXYLASE	1.46e+00
16	61	41.8	594	1 DCE1_HUMAN	GLUTAMATE DECARBOXYLASE	1.46e+00
17	61	41.8	770	1 YR9Y_CAEEL	HYPOTHETICAL 84.2 KD P	1.46e+00
18	59	40.4	133	1 YB88_YEAST	HYPOTHETICAL 15.5 KD P	3.54e+00
19	58	39.7	926	1 CLAA_LYCES	ATP-DEPENDENT CLP PROTEIN	5.45e+00
20	58	39.7	361	1 TRMU_CHLUP	PROBABLE TRNA (5-METHYL)	5.45e+00
21	58	39.7	488	1 CAFA_ECOLI	CYTOPLASMIC AXIAL FILAMENT	5.45e+00
22	58	39.7	650	1 APPI_HUMAN	AMYLOID-LIKE PROTEIN 1	5.45e+00
23	58	39.7	653	1 APPI_MOUSE	AMYLOID-LIKE PROTEIN 1	5.45e+00

24	58	39.7	663	1 ALOX_CANBO	ALCOHOL OXIDASE (EC 1.1.3.1)	5.45e+00
25	58	39.7	1394	1 CNG4_BOVIN	240 KD PROTEIN OF ROD	5.45e+00
26	58	39.7	1677	1 VIT1_ACITR	VITELLOGENIN PRECURSOR	5.45e+00
27	57	39.0	288	1 YDO9_SCHPO	HYPOTHETICAL 31.5 KD P	8.36e+00
28	57	39.0	462	1 FUMH_BACSU	FUMARATE HYDRATASE, CL	8.36e+00
29	57	39.0	523	1 SRC_RSVPA	TYROSINE-PROTEIN KINASE	8.36e+00
30	57	39.0	526	1 SRC_RSVSR	TYROSINE-PROTEIN KINASE	8.36e+00
31	57	39.0	526	1 SRC_AVISR	TYROSINE-PROTEIN KINASE	8.36e+00
32	57	39.0	540	1 GRBE_HUMAN	GROWTH FACTOR RECEPTOR	8.36e+00
33	57	39.0	582	1 PME2_ARATH	PECTINESTERASE 2 (EC 3.1.1.1)	8.36e+00
34	57	39.0	584	1 PME1_CITSI	PECTINESTERASE 1.1 PRE	8.36e+00
35	57	39.0	848	1 AHR_HUMAN	AH RECEPTOR (ARYL HYDRO	8.36e+00
36	57	39.0	853	1 AHR_RAT	AH RECEPTOR (ARYL HYDRO	8.36e+00
37	57	39.0	876	1 YNE9_YEAST	HYPOTHETICAL 98.9 KD P	8.36e+00
38	56	38.4	498	1 YAC3_SCHPO	HYPOTHETICAL 56.6 KD P	1.27e+01
39	56	38.4	637	1 MUTA_PROPR	METHYLMALONYL-COA MUTA	1.27e+01
40	56	38.4	646	1 PLAP_MOUSE	PHOSPHOLIPASE A-2-ACTI	1.27e+01
41	56	38.4	647	1 PLAP_RAT	PHOSPHOLIPASE A-2-ACTI	1.27e+01
42	56	38.4	909	1 CNG4_HUMAN	CYCLOC-NUCLEOTIDE GATE	1.27e+01
43	56	38.4	4568	1 DYHC_CAEEL	DYNEIN HEAVY CHAIN, CY	1.27e+01
44	55	37.7	174	1 Y030_BPHP1	HYPOTHETICAL 20.8 KD P	1.93e+01
45	55	37.7	1274	1 BXF_CLOBO	BOTULINUM NEUROTOXIN T	1.93e+01

## ALIGNMENTS

RESULT ID	1	DCE2_HUMAN	STANDARD:	PRT:	585 AA.
AC	005329:				
DT	01-FEB-1996	(Rel. 33, Created)			
DT	01-FEB-1996	(Rel. 33, Last sequence update)			
DT	01-FEB-1996	(Rel. 33, Last annotation update)			
DE	GLUTAMATE DECARBOXYLASE, 65 KD ISOFORM (EC 4.1.1.15) (GAD-65)				
DE	(65 KD GLUTAMIC ACID DECARBOXYLASE).				
GN	GAD2 OR GAD65.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;				
OC	Eutheria; Primates; Catarrhini; Hominiidae; Homo.				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE: 92196068.				
RA	BU D.-F., ERLANDER M.G., HITZ B.C., TILLAKRATNE N.J., KAUFMAN D.L.,				
RA	WAGNER-MCPHERSON C.B., EVANS G.A., TOBIN A.J.;				
RT	"Two human glutamate decarboxylases, 65-kDa GAD and 67-kDa GAD, are				
RT	each encoded by a single gene."				
RL	Proc. Natl. Acad. Sci. U.S.A. 89:2115-2119(1992).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE: 94375018.				
RA	BU D.-F., TOBIN A.J.;				
RT	"The exon-intron organization of the genes (GAD1 and GAD2) encoding				
RT	two human glutamate decarboxylases (GAD67 and GAD65) suggests that				
RT	they derive from a common ancestral GAD."				
RL	Genomics 21:222-228(1994).				
RN	[3]				
RP	SEQUENCE FROM N.A.				
RX	TISSUE-PANCREATIC ISLETS;				
RA	KARLSN A.E., BARKEIER H., MATHEWS S., GRANT F.J., FOSTER D.,				
RA	ADLER D.A., HARGOPIN W.A., GRUBIN C.E., DUBE S., DISTECHE C.M.,				
RA	LEHMARK A.;				
RT	"Cloning and primary structure of a human islet isoform of glutamic				
RT	acid decarboxylase from chromosome 10."				
RL	Proc. Natl. Acad. Sci. U.S.A. 88:8337-8341(1991).				
RN	[4]				
RP	SEQUENCE OF 6-585 FROM N.A.				
RX	TISSUE-PANCREAS;				
RA	MEDLINE: 93185681.				
RA	MAUCH L., ABNEY C.C., BERG H., SCHERBAUM W.A., LEDVOGEL B.,				
RA	NORTHMAN W.;				
RT	"Characterization of a linear epitope within the human pancreatic				
RT	64-kDa glutamic acid decarboxylase and its autoimmune recognition by				
RT	sera from insulin-dependent diabetes mellitus patients."				

```

RL Eur. J. Biochem. 212:597-603(1993).
CC -1- FUNCTION: CATALYZES THE PRODUCTION OF GABA.
CC -1- CATALYTIC ACTIVITY: L-GLUTAMATE = 4-AMINOBUTANATE + CO(2).
CC -1- COFACTOR: PYRIDOXAL PHOSPHATE.
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SIMILARITY: LOCAL TO DOPA DECARBOXYLASE, AND TO PLP-TYPE HISTIDINE
CC DECARBOXYLASE.
-----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
-----
CC EMBL: M81882; AAA62367.1; -
CC EMBL: M74826; AAA58491.1; -
CC EMBL: X69936; CAA49554.1; ALT_INIT.
CC EMBL: M70435; AAA52513.1; -
CC PIR: A41292; A41292.
CC PIR: PQ0158; PQ0158.
CC MIM: 138275; -
CC DR PROSITE: PS00392; DDC_GAD_HDC_YDC; 1.
CC DR PFAM: PF00282; Pyridoxal_dec; 1.
CC KW Neurotransmitter biosynthesis; Lyase; Decarboxylase;
CC KM Pyridoxal phosphate; Multigene family.
CC FT BINDING 396 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
CC SQ SEQUENCE 585 AA; 65411 MW; 8AD62B62 CRC32;

Query Match 100.0%; Score 146; DB 1; Length 585;
Best Local Similarity 100.0%; Pred. No. 7.49e-22;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 86 DVMYAFIHMATDLPACDGER 105
QY 1 DVMYAFIHMATDLPACDGER 20
|||||
RESULT 2
AC DCE2_MOUSE STANDARD; PRT; 585 AA.
P48320; 035519;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE GLUTAMATE DECARBOXYLASE, 65 KD ISOFORM (EC 4.1.1.15) (GAD-65)
DE (65 KD GLUTAMIC ACID DECARBOXYLASE).
DE GN GAD2 OR GAD65.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-C57BL/6; TISSUE-BRAIN;
RX MEDLINE: 94032481.
RX LEE D.S., TIAN J., PHAN T., KAUFMAN D.L.;
RT Cloning and sequence analysis of a murine cDNA encoding glutamate
RT decarboxylase (GAD65).
RL Biochim. Biophys. Acta 1216:157-160(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-C57BL/6; TISSUE-BRAIN;
RX MEDLINE: 97115675.
RX ASADA H., KAWAMURA Y., NARUYAMA K., KUME H., DING R.G., JI F.Y.,
RX KANBARA N., KUZUME H., SANBO M., YAGI T., OBATA K.;
RT "Mice lacking the 65 kDa isoform of glutamic acid decarboxylase
RT (GAD65) maintain normal levels of GAD67 and GABA in their brains but
RT are susceptible to seizures."
RL Biochem. Biophys. Res. Commun. 229:891-895(1996).
RN [3]
RP SEQUENCE OF 175-379 FROM N.A.
RC TISSUE-BRAIN;
RX MEDLINE: 94062679.

```

```

RA FAULKNER-JONES B.E., CRAW D.S., KUN J., HARRISON L.C.;
RT "Localization and quantitation of expression of two glutamate
RT decarboxylase genes in pancreatic beta-cells and other peripheral
RT tissues of mouse and rat."
RL Endocrinology 133:2962-2972(1993).
CC -1- FUNCTION: CATALYZES THE PRODUCTION OF GABA.
CC -1- CATALYTIC ACTIVITY: L-GLUTAMATE = 4-AMINOBUTANATE + CO(2).
CC -1- CORRECTOR: PYRIDOXAL PHOSPHATE.
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SIMILARITY: LOCAL TO DOPA DECARBOXYLASE, AND TO PLP-TYPE HISTIDINE
CC DECARBOXYLASE.
-----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
-----
CC EMBL: L16980; AAA93049.1; -
CC EMBL: D42051; BAA22893.1; -
CC EMBL: S67454; CAB32806.1; -
CC MGD: MGI:95634; GAD2.
CC DR PROSITE: PS00392; DDC_GAD_HDC_YDC; 1.
CC DR PFAM: PF00282; Pyridoxal_dec; 1.
CC KW Neurotransmitter biosynthesis; Lyase; Decarboxylase;
CC KM Pyridoxal phosphate; Multigene family.
CC FT BINDING 396 PYRIDOXAL PHOSPHATE (POTENTIAL).
CC FT CONFLICT 259 259 F -> S (IN REF. 2).
CC FT CONFLICT 319 319 I -> S (IN REF. 3).
CC FT CONFLICT 325 325 K -> E (IN REF. 2).
CC FT CONFLICT 499 499 P -> S (IN REF. 2).
CC SQ SEQUENCE 585 AA; 65224 MW; 9B5C088 CRC32;

Query Match 100.0%; Score 146; DB 1; Length 585;
Best Local Similarity 100.0%; Pred. No. 7.49e-22;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 86 DVMYAFIHMATDLPACDGER 105
QY 1 DVMYAFIHMATDLPACDGER 20
|||||
RESULT 3
AC DCE2_PIG STANDARD; PRT; 585 AA.
P48321;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE GLUTAMATE DECARBOXYLASE, 65 KD ISOFORM (EC 4.1.1.15) (GAD-65)
DE (65 KD GLUTAMIC ACID DECARBOXYLASE).
DE GN GAD2 OR GAD65.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Cetartiodactyla; Suidae; Sus.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RX MEDLINE: 95137399.
RX SUZUKI R., ASAMI N., AMANN E., WAGATSUMA M.;
RT Sequences of two porcine glutamic acid decarboxylases (65- and
RT 67-kDa GAD).
RL Gene 152:257-260(1995).
CC -1- FUNCTION: CATALYZES THE PRODUCTION OF GABA.
CC -1- CATALYTIC ACTIVITY: L-GLUTAMATE = 4-AMINOBUTANATE + CO(2).
CC -1- CORRECTOR: PYRIDOXAL PHOSPHATE.
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO GROUP II DECARBOXYLASES (DDC, GAD, HDC AND
CC TYRDC).
-----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

```







```

SQ  SEQUENCE 2616 AA: 292371 MW: 0FDF8412 CRC32;
Query Match: 43.8%; SCORE 64; DB 1; Length 2616;
Best Local Similarity 47.1%; Pred. No. 3,72e+01;
Matches 8; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Db 2390 FTYLQATDPSPKICDGR 2406
:::1111 1111
4 YAFHATIDLLPACDGER 20

RESULT 9
ID KPAT UMW4 STANDARD; PRT: 127 AA.
AC O90121;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE KP4 KILLER TOXIN PRECURSOR.
GN M2A.
OS Ustilago maydis P4 virus (UMV4) (UMV-P4).
OC Viruses; dsRNA viruses; Totiviridae; Totivirus.
RN (1)
RP SEQUENCE FROM N.A., AND SEQUENCE OF 23-79 AND 124-127.
RC STRAIN-77;
RX MEDLINE: 94195103.
RA PARK C.-M., BRUENN J.A., GANESA C., FLURKEY W.F., BOZARTH R.F.,
RA KOLPIN Y.;
RT "Structure and heterologous expression of the Ustilago maydis viral
RT toxin KP4.";
RL Mol. Microbiol. 11:155-164(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-M2B;
RX GU F., KHMANT A.K., FLURKEY W.F., BOZARTH R.F., SMITH T.J., RANE S.;
RL Submitted (SEP-1995) to the EMBL/Genbank/DBJ databases.
RN [3]
RP CHARACTERIZATION AND SEQUENCE OF 23-52.
RX MEDLINE: 91378286.
RA GANESA C., FLURKEY W.H., RANDHAWA Z.I., BOZARTH R.F.;
RT "Ustilago maydis virus P4 killer toxin: characterization, partial
RT amino terminus sequence, and evidence for glycosylation.";
RL Arch. Biochem. Biophys. 286:195-200(1991).
RN [4]
RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
RX MEDLINE: 96021102.
RA GU F., KHMANT A., RANE S.G., FLURKEY W.H., BOZARTH R.F., SMITH T.J.;
RT "Structure and function of a virally encoded fungal toxin from
RT Ustilago maydis: a fungal and mammalian Ca2+ channel inhibitor.";
RL Structure 3:805-814(1995).
CC -!- FUNCTION: THIS PROTEIN IS LETHAL TO SENSITIVE CELLS OF THE SAME OR
CC RELATED SPECIES. IT SPECIFICALLY INHIBITS VOLTAGE-GATED CALCIUM
CC CHANNELS. KILLS TARGET FUNGAL CELLS BY BLOCKING DIVALENT CATION
CC CHANNELS (VIA CALCIUM AND/OR MAGNESIUM CHANNELS).
CC -!- SUBUNIT: MONOMER.
CC -!- SUBCELLULAR LOCATION: SECRETED.
CC -!- MASS SPECTROMETRY: MW=11045; MW-ERR=11; METHOD=MALDI;
CC RANGE=23-127.
CC -!- CAUTION: WAS SAID BY REF.3 TO BE GLYCOSYLATED, BUT THIS DOES NOT
CC SEEM TO BE THE CASE ACCORDING TO REF.1.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: L12226; AAA89185.1; -.
CC EMBL: U25179; AAA75041.1; -.
CC PDB: 1KPT; 31-OCT-95.
CC Toxin; Signal; 3D-structure.
CC SIGNAL 1 22

```

FT	CHAIN	23	127		KP4 KILLER TOXIN.
FT	DISULFID	27	100		
FT	DISULFID	33	103		
FT	DISULFID	49	89		
FT	DISULFID	57	82		
FT	DISULFID	66	127		
FT	CONFLICT	56	56	W -> I (IN AA SEQUENCE; REF. 1).	
FT	CONFLICT	66	66	C -> E (IN AA SEQUENCE; REF. 1).	
FT	CONFLICT	67	67	G -> C (IN AA SEQUENCE; REF. 1).	
FT	CONFLICT	73	73	S -> D (IN AA SEQUENCE; REF. 1).	
FT	CONFLICT	74	74	A -> H (IN AA SEQUENCE; REF. 1).	
FT	CONFLICT	79	79	T -> S (IN AA SEQUENCE; REF. 1).	
SO	SEQUENCE	127 AA;	13489 MW;	AF63PB09 CRC32;	
Query Match					
Best Local Similarity		43.2%;	Score 63;	DB 1;	Length 127;
Matches		7; Conservative	4; Mismatches	3; Indels	0; Gaps
Db	5	NYVYSFLFAAMLP	18		
Qy	1	DVNYAFHLATDLP	14		
RESULT					
ID	10	STANDARD;	PRT;	396 AA.	
AC	P55579.				
DT	01-NOV-1997	(Rel. 35, Created)			
DT	01-NOV-1997	(Rel. 35, Last sequence update)			
DT	01-NOV-1997	(Rel. 35, Last annotation update)			
DE	HYPOTHETICAL 42.8 KD PROTEIN YANG.				
GN	YANG.				
OS	Rhizobium sp. (strain NGR234).				
OC	Plasmid sym PNG234a.				
OC	Bacteria; Proteobacteria; alpha subdivision: Rhizobiaceae group;				
OC	Rhizobiaceae; Rhizobium.				
	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE; 97305956.				
RA	FRIEBERG C.A., FELLAY R., BAIROCH A., BROUGHTON W.J., ROSENTHAL A.,				
RA	PERRET X.;				
RL	"Molecular basis of symbiosis between Rhizobium and legumes.";				
	Nature 387:394-401(1997).				
CC	-I- FUNCTION: PUTATIVE NUCLEOTIDE SUGAR EPIMERASE/DEHYDROGENASE.				
CC	-I- COPACTOR: NAD OR NADP.				
CC	-I- SIMILARITY: SOME, TO UDP-GLUCOSE 4-EPIMERASE (EC 5.1.3.2),				
CC	DDDP-GLUCOSE 4,6-DEHYDRATASE (EC 4.2.1.46) AND NAD(P)-DEPENDENT				
CC	CHOLESTEROL DEHYDROGENASES.				
	-----				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration				
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -				
CC	the European Bioinformatics Institute. There are no restrictions on its				
CC	use by non-profit institutions as long as its content is in no way				
CC	modified and this statement is not removed. Usage by and for commercial				
CC	entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a>				
CC	or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).				
	-----				
CC	EMBL; AE000087; AAB91786.1; -				
DR	PFAM; PF01370; Epimerase; 1.				
KW	Hypothetical protein; NAD; Plasmid.				
SO	SEQUENCE 396 AA; 42842 MW; 58CCTDDE CRC32;				
Query Match					
Best Local Similarity		43.2%;	Score 63;	DB 1;	Length 396;
Matches		7; Conservative	4; Mismatches	3; Indels	0; Gaps
Db	243	KYGFVHSDDLASAC	256		
Qy	3	NYAFHLATDLPAC	16		
RESULT					
ID	11	STANDARD;	PRT;	533 AA.	
AC	P08997.				

DT 01-NOV-1988 (Rel. 09, Created)  
DT 01-NOV-1988 (Rel. 09, Last sequence update)  
DT 15-DEC-1999 (Rel. 39, Last annotation update)  
DE MALATE SYNTHASE A (EC 4.1.3.2) (MSA).  
GN ACCEB OR MAS.  
OS Escherichia coli.  
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
OC Escherichia.  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-K12;  
RX MEDLINE: 89016638.  
RA BYRNE C.R., STOKES H.W., WARD K.A.;  
RT "Nucleotide sequence of the aceB gene encoding malate synthase A in  
RT Escherichia coli.";  
RL Nucleic Acids Res. 16:9342-9342(1988).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN-K12 / MG1655;  
RX MEDLINE: 94089392.  
RA BLATTNER F.R., BURLAND V.D., PLUNKETT G. III, SOFIA H.J.,  
RA DANIELS D.L.;  
RT "Analysis of the Escherichia coli genome. IV. DNA sequence of the  
RT region from 89.2 to 92.8 minutes.";  
RL Nucleic Acids Res. 21:5408-5417(1993).  
CC -1- CATALYTIC ACTIVITY: L-MALATE + COA -> ACETYL-COA + H(2)O +  
CC GLYOXYLATE.  
CC -1- PATHWAY: SECOND STEP IN GLYOXYLATE BYPASS, AN ALTERNATIVE TO THE  
CC TRICARBOXYLIC ACID CYCLE (IN BACTERIA, FUNGI AND PLANTS).  
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.  
CC -1- SIMILARITY: BELONGS TO THE MALATE SYNTHASE FAMILY.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL: X12431; CA030973.1; -;  
DR EMBL: U000006; AAC43108.1; -;  
DR EMBL: AE000474; AAC76984.1; -;  
DR PIR: Q00592; SYEDMA.  
DR ECGENE: EG10023; ACEB.  
DR PROSITE: PS00510; MALATE\_SYNTHASE: 1.  
DR PFM: PF01274; Malate\_synthase: 1.  
KW Glyoxylate bypass; Tricarboxylic acid cycle; Lyase.  
SQ SEQUENCE 533 AA; 60273 MW; C805B9F8 CRC32;  
Query Match 43.2%; Score 63; DB 1; Length 533;  
Best Local Similarity 66.7%; Pred. No. 5.90e-01;  
Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
Db 402 ADOLAPCDGER 413  
Qy 9 ATDLPCADGER 20  
RESULT 12  
ID DCEL\_MOUSE STANDARD: PRT: 593 AA.  
AC P48318.  
DT 01-FEB-1996 (Rel. 33, Created)  
DT 01-FEB-1996 (Rel. 33, Last sequence update)  
DT 01-FEB-1996 (Rel. 33, Last annotation update)  
DE GLUTAMATE DECARBOXYLASE. 67 KD ISOFORM (EC 4.1.1.15) (GAD-67)  
DE (67 KD GLUTAMIC ACID DECARBOXYLASE).  
GN GADI OR GAD67.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
RN [1]  
RP SEQUENCE FROM N.A.  
RX

RC TISSUE-BRAIN.  
RA KATAROVA Z., SZABO G., MUGNAINI E., GREENSPAN R.;  
RT "Molecular identification of the 62 kd form of glutamic acid  
RT decarboxylase from the mouse.";  
RL Eur. J. Neurosci. 2:190-202(1990).  
RN [2]  
RP SEQUENCE OF 198-403 FROM N.A.  
RC TISSUE-BRAIN.  
RX MEDLINE: 94062679.  
RA FAULKNER-JONES B.E., GRAM D.S., KUN J., HARRISON L.C.;  
RT "Localization and quantitation of expression of two glutamate  
RT decarboxylase genes in pancreatic beta-cells and other peripheral  
RT tissues of mouse and rat.";  
RL Endocrinology 133:2962-2972(1993).  
CC -1- FUNCTION: CATALYZES THE PRODUCTION OF GABA.  
CC -1- CATALYTIC ACTIVITY: L-GLUTAMATE -> 4-AMINOBUTANOATE + CO(2).  
CC -1- COFACTOR: PYRIDOXAL PHOSPHATE.  
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).  
CC -1- SIMILARITY: BELONGS TO GROUP II DECARBOXYLASES (DDC, GAD, HDC AND  
CC TYRDC).  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL: Z49976; CA90277.1; -;  
DR EMBL: S67453; CAB32805.1; -;  
DR MGD: MGI:95632; GADI.  
DR PROSITE: PS00392; DDC\_GAD\_HDC\_YDC: 1.  
DR PFM: PFO0282; Pyridoxal\_dec: 1.  
KW Neurotransmitter biosynthesis; Lyase; Decarboxylase;  
KW Pyridoxal phosphate; Multigene family.  
FT BINDING 404 404 PYRIDOXAL PHOSPHATE (POTENTIAL).  
FT CONFLICT 234 234 E -> K (IN REF. 2).  
FT CONFLICT 258 258 S -> T (IN REF. 1).  
FT CONFLICT 360 360 D -> S (IN REF. 1).  
SQ SEQUENCE 593 AA; 66584 MW; 63BC57AA CRC32;  
Query Match 41.8%; Score 61; DB 1; Length 593;  
Best Local Similarity 47.4%; Pred. No. 1.46e+00;  
Matches 9; Conservative 5; Mismatches 5; Indels 0; Gaps 0;  
Db 91 ETDPSNLFADLLPAKNCE 109  
Qy 1 DVNFAFLHATDLPCDGE 19  
RESULT 13  
ID DCEL\_RAT STANDARD: PRT: 593 AA.  
AC P18088.  
DT 01-NOV-1990 (Rel. 16, Created)  
DT 01-NOV-1990 (Rel. 16, Last sequence update)  
DT 01-FEB-1996 (Rel. 33, Last annotation update)  
DE GLUTAMATE DECARBOXYLASE. 67 KD ISOFORM (EC 4.1.1.15) (GAD-67)  
DE (67 KD GLUTAMIC ACID DECARBOXYLASE).  
GN GADI OR GAD67.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE: 91014554.  
RA WYBORSKI R.J., BOND R.W., GOTTLIEB D.I.;  
RT "Characterization of a cDNA coding for rat glutamic acid  
RT decarboxylase.";  
RL Brain Res. Mol. Brain Res. 8:193-198(1990).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE: 90132703.





DR PROSITE: PS00392; DDC\_GAD\_HDC\_YDC; 1.  
DR PRAM: PF00282; Pyridoxal\_dec; 1.  
KW Neurotransmitter biosynthesis; Lyase; Decarboxylase;  
KW Pyridoxal phosphate; Multigene family.  
FT BINDING 405 405 PYRIDOXAL PHOSPHATE (POTENTIAL).  
SQ SEQUENCE 594 AA: 66824 MW: 3620778 CRC32;

Query Match 41.8%; Score 61; DB 1; Length 594;  
Best Local Similarity 47.4%; Pred. No. 1.46e+00;  
Matches 9; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Lb 92 ETDSNLFARDLPAKNGE 110  
QY 1 DVNYAFLLHATDLPACDGE 19

Search completed: Tue Mar 7 21:02:42 2000  
Job time : 5 secs.

**THIS PAGE BLANK (USPTO)**

回 回 回 回 回

(TM)

OC Eutheria; Primates; Catarrhini; Cercopithecoidea; Cercopithecinae;  
OC Macaca.  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE: 96256692.  
RA MITSUSHIMA D., MARZBAN F., LUCHANSKY L.L., BURICH A.J., KEEN K.L.,  
RA DUNNING M., GOLOS T.G., TERASAWA E.;  
RT "Role of glutamic acid decarboxylase in the prepubertal inhibition of  
the luteinizing hormone releasing hormone release in female rhesus  
monkeys."  
RL J. Neurosci. 16:2563-2573(1996).  
DR EMBL: S82650; AAB46786.1; -  
FT NON TER 1  
SQ SEQUENCE 76 AA: 8143 MW: 1AB755D0 CRC32:  
DB 44 DILLPACDGER 53  
OY 11 DILLPACDGER 20  
RESULT 3  
ID 09WT57 PRELIMINARY: PRT: 374 AA.  
AC 09WT57;  
DT 01-NOV-1999 (TREMBLrel. 12, Created)  
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)  
DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)  
DE 97.3% IDENTICAL TO U7 GENE OF STRAIN U1102 OF HHV-6.  
GN U7.  
OS Human herpesvirus 6.  
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;  
OC Betaherpesvirinae; Roseolovirus.  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-HST:  
RA ISEGAWA Y., NUKAI T., NAKANO K., KAGAWA M., CHEN J., MORI Y.,  
RA SUNAGAWA T., SASIHARA J., ZOU P., KOSUGE H., YAMANISHI K.;  
RT "A comparison of the complete DNA sequences between human herpesvirus-  
RT 6 variant A and B."  
RL J. Virol. 0:0-0(1999).  
DR EMBL: AB021506; BAA78227.1; -  
SQ SEQUENCE 374 AA: 43081 MW: 3588A75C CRC32:  
Query Match 46.6%; Score 68; DB 14; Length 374;  
Best Local Similarity 33.3%; Pred. No. 3,92e+01;  
Matches 6; Conservative 8; Mismatches 4; Indels 0; Gaps 0;  
DB 23 LHFAPFQTEIVPCNDE 40  
OY 2 VNYAFLEHATDLPACDGE 19  
RESULT 4  
ID 09Y0E4 PRELIMINARY: PRT: 2262 AA.  
AC 09Y0E4;  
DT 01-NOV-1999 (TREMBLrel. 12, Created)  
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)  
DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)  
DE KLASISCHT PROTEIN.  
GN KLAS.  
OS Drosophila melanogaster (Fruit fly).  
OC Eukaryota; Metazoa; Anthropoda; Tracheata; Hexapoda; Insecta;  
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
CC Ephydroidea; Drosophilidae; Drosophila.  
RN [1]  
RP SEQUENCE FROM N.A.  
RA MOSLEY-BISHOP K.L., LI Q., PATTERSON K., FISCHER J.A.;  
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF157066; AAD43129.1; -  
SQ SEQUENCE 2262 AA: 245116 MW: E35504F7 CRC32:

Query Match 45.2%; Score 66; DB 5; Length 2262;  
Best Local Similarity 33.0%; Pred. No. 9,23e+01;  
Matches 7; Conservative 5; Mismatches 8; Indels 0; Gaps 0;  
DB 225 QTNVYIMDTNLDPTCKEAR 244  
OY 1 DNYAFLEHATDLPACDGER 20  
RESULT 5  
ID 09WVG7 PRELIMINARY: PRT: 266 AA.  
AC 09WVG7;  
DT 01-NOV-1999 (TREMBLrel. 12, Created)  
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)  
DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)  
DE ODD-SKIPPED RELATED 1 PROTEIN.  
GN OSR1.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE: 9940011.  
RA SO P.L., DANIELIAN P.S.;  
RT "Cloning and expression analysis of a mouse gene related to Drosophila  
RT odd-skipped."  
RL Mech. Dev. 84:157-160(1999).  
DR EMBL: AF117814; AAD37115.1; -  
DR PROSITE: PS00028; ZINC\_FINGER\_C2H2\_3.  
KW Zinc-finger; Metal-binding; DNA-binding  
SQ SEQUENCE 266 AA: 29584 MW: 8A97D286 CRC32:  
Query Match 43.8%; Score 64; DB 11; Length 266;  
Best Local Similarity 38.9%; Pred. No. 2,13e+00;  
Matches 7; Conservative 7; Mismatches 4; Indels 0; Gaps 0;  
DB 20 NYSFLQAVNGIPTVPSDR 37  
OY 3 NYAFLEHATDLPACDGER 20  
RESULT 6  
ID 09Y158 PRELIMINARY: PRT: 590 AA.  
AC 09Y158;  
DT 01-MAY-1999 (TREMBLrel. 10, Created)  
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)  
DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)  
DE GLUTAMATE DECARBOXYLASE 67.  
GN GAD67.  
OS Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;  
OC Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=WHITE LEGHORN;  
RA WAGBERG F.;  
RT "Characterization of glutamate decarboxylase in chicken."  
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.  
CC -I- COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).  
CC -I- SIMILARITY: BELONGS TO GROUP II DECARBOXYLASES (DDC, GAD, HDC AND  
CC TYRDC).  
DR EMBL: AF030355; AAD01902.1; -  
DR PROSITE: PS00392; DDC\_GAD\_HDC\_YDC\_1.  
KW Lysase; Decarboxylase; Pyridoxal phosphate.  
SQ SEQUENCE 590 AA: 66710 MW: 80B66DFE CRC32:  
Query Match 43.8%; Score 64; DB 13; Length 590;  
Best Local Similarity 47.4%; Pred. No. 2,13e+00;  
Matches 9; Conservative 5; Mismatches 5; Indels 0; Gaps 0;  
DB 88 ETDPSNLVARDLPAKNGE 106  
: : : : : | | | | | : | |

OY 1 DVNVAFLHATDLPACDGE 19

```

RESULT 7
ID Q020297 PRELIMINARY: PRT: 277 AA.
AC Q020297
DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
DT 01-NOV-1998 (TREMblrel. 08, Last annotation update)
DE COSMID F41H10.
GN F41H10.5.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
OC Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RX MEDLINE: 94150718.
RA WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
RA BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,
RA CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULLON L.,
RA GARDNER A., GREEN P., HAWKINS T., KIRSTEN J., LAISTER N., LATREILLE P.,
RA GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
RA JONES M., KERSHAW J., KIRSHEN J., LAISTER N., LATREILLE P.,
RA LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
RA PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
RA SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULLSTON J.,
RA THERRRY-MEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
RA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans."
RL Nature 368:32-38(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA BLANCHARD M., BRADSHAW H.;
RN Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA WATERSTON R.;
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL: U61954; AAB03172.1; -
SO SEQUENCE 277 AA; 32024 MW; E8B04CAD CRC32;

Query Match 43.2%; Score 63; DB 5; Length 277;
Best Local Similarity 50.0%; Pred. No. 3.23e+00;
Matches 8; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Db 162 EVNSFLHARTDLPAC 177
OY 1 DVNVAFLHATDLPAC 16

RESULT 8
ID Q046012 PRELIMINARY: PRT: 329 AA.
AC Q046012
DT 01-JUN-1998 (TREMblrel. 06, Created)
DT 01-JUN-1998 (TREMblrel. 06, Last sequence update)
DT 01-NOV-1999 (TREMblrel. 12, Last annotation update)
DE ZK228.7 PROTEIN.
GN ZK228.7.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
OC Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
RN [1]
RP SEQUENCE FROM N.A.
RC BASHAM V.;
RN Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC MEDLINE: 94150718.
RA WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
RA BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,

```

```

RA CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULLON L.,
RA GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
RA JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
RA LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
RA PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
RA SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULLSTON J.,
RA THERRRY-MEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
RA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans."
RL Nature 368:32-38(1994).
DR EMBL: 282086; CAB04998.1; -
DR PFM: PF01604; 7tm_5; 1.1.
SO SEQUENCE 329 AA; 36804 MW; 5E81A635 CRC32;

Query Match 43.2%; Score 63; DB 5; Length 329;
Best Local Similarity 52.6%; Pred. No. 3.23e+00;
Matches 10; Conservative 3; Mismatches 5; Indels 1; Gaps 1;

Db 63 DVESFLAPVLTLPDGC 81
OY 1 DVNVAFLHATDLPACDG 18

RESULT 9
ID Q25107 PRELIMINARY: PRT: 150 AA.
AC Q25107
DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
DT 01-NOV-1999 (TREMblrel. 12, Last annotation update)
DE LYSIN PRECURSOR.
OS Halobacterium salinarum.
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Archaeogastropoda;
OC Haliotidae; Haliotis.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-TESTIS;
RA LEE Y.H., VACQUIER V.D.;
RL Submitted (NOV-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL: L26276; AAA21522.1; -
DR HSSP: P04552; ILYN.
DR PFM: PF01303; Egg_Lysin; 1.
KW Signal.
FT SIGNAL 1 18 POTENTIAL.
FT CHAIN 19 150 LYSIN.
SO SEQUENCE 150 AA; 17691 MW; 546D9513 CRC32;

Query Match 42.5%; Score 62; DB 5; Length 150;
Best Local Similarity 50.0%; Pred. No. 4.86e+00;
Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Db 117 EVNSFLVRRNLP 130
OY 1 DVNVAFLHATDLP 14

RESULT 10
ID Q926P6 PRELIMINARY: PRT: 460 AA.
AC Q926P6
DT 01-MAY-1999 (TREMblrel. 10, Created)
DT 01-MAY-1999 (TREMblrel. 10, Last sequence update)
DT 01-NOV-1999 (TREMblrel. 12, Last annotation update)
DE FUMARATE HYDRATASE.
GN FUMC.
OS Chlamydia pneumoniae.
OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CWL029;
RA KALMAN S., MITCHELL W., MARATHE R., LAMMEL C., FAN J., OLINGER L.,
RA GRIMWOOD J., DAVIS R.W., STEPHENS R.S.;
RT "Comparative Genomes of Chlamydia pneumoniae and C. trachomatis."
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.

```

DR EMBL: AE001681; AAD19150.1; -  
 DR HSSP: P05042; 1FUO;  
 DR PROSITE: PS00163; FUMARATE\_LYASES; 1;  
 SQ SEQUENCE 460 AA; 50441 MW; AA418380 CRC32;

Query Match 42.5%; Score 62; DB 2; Length 460;  
 Best Local Similarity 46.2%; Pred. No. 4.86e+00;  
 Matches 6; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Db 362 IITNFIQSVDDL 374  
 : 111:111:  
 QY 2 DVNYAFIATDLPACD 14

RESULT 11  
 ID 008465 PRELIMINARY; PRT; 219 AA.  
 AC 008465; 000025;  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)  
 DE CHROMOSOME XV READING FRAME ORF YOR064C.  
 GN YOR29-15.  
 OS Saccharomyces cerevisiae (Baker's yeast).  
 OC Eukaryota; Fungi; Ascomycota; Hemiascomycetes; Saccharomycetales;  
 OC Saccharomycetaceae; Saccharomyces.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA BOHN C., BOLOTIN-FUKUHARA M., DAIGNAN-FORNIER B., DANG D.V.,  
 RA VALENS M.;  
 RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA MIPS;  
 RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE: 97279235.  
 RA VALENS M., BOHN C., DAIGNAN-FORNIER B., DANG V., BOLOTIN-FUKUHARA M.;  
 RT "The sequence of a 54.7 kb fragment of yeast chromosome XV reveals the  
 presence of two tRNAs and 24 new open reading frames."  
 RL Yeast 13:379-390(1997).  
 DR EMBL: 274972; CAA99257.1; -  
 DR EMBL: 270678; CAA94549.1; -  
 DR PRAM: PF00628; PHD; 1  
 SQ SEQUENCE 219 AA; 25350 MW; 1119F5E2 CRC32;

Query Match 41.8%; Score 61; DB 3; Length 219;  
 Best Local Similarity 47.1%; Pred. No. 7.28e+00;  
 Matches 8; Conservative 4; Mismatches 4; Indels 1; Gaps 1;

Db 12 DIRSFLSTDHP-CE 27  
 : 111:111:  
 QY 1 DVNYAFIATDLPACD 17

RESULT 12  
 ID 063211 PRELIMINARY; PRT; 223 AA.  
 AC 063211;  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)  
 DE GLUTAMATE DECARBOXYLASE.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE: 91062362.  
 RA BOND R.W., WYBORSKI R.J., GOTTLIEB D.I.;  
 RT "Developmentally regulated expression of an exon containing a stop  
 codon in the gene for glutamic acid decarboxylase."  
 RL Proc. Natl. Acad. Sci. U.S.A. 87:8771-8775(1990).  
 DR EMBL: M38350; AAA41185.1; -

DR PRAM: PF00282; pyridoxal dec; 1.  
 SQ SEQUENCE 223 AA; 25069 MW; C7162AC1 CRC32;

Query Match 41.8%; Score 61; DB 11; Length 223;  
 Best Local Similarity 47.4%; Pred. No. 7.28e+00;  
 Matches 9; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Db 91 EITFSLFAODLIPACGE 109  
 : 1111111111:  
 QY 1 DVNYAFIATDLPACDGE 19

RESULT 13  
 ID 042504 PRELIMINARY; PRT; 236 AA.  
 AC 042504;  
 DT 01-JAN-1998 (TREMBLrel. 05, Created)  
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)  
 DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)  
 DE HOMEBOX PROTEIN HOXC-6.  
 GN ERHOXC-6.  
 OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;  
 OC Neopterygii; Teleostei; Euteleostei; Acanthopterygii; Percomorpha;  
 OC Tetraodontiformes; Tetraodontidae; Tetraodontidae; Fugu.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE: 97285126.  
 RA APARICIO S., HAWKER K., COTTAGE A., MIKAWA Y., ZUO L., VENKATESH B.,  
 RA CHEN E., KRUMLAUF R., BRENNER S.;  
 RT "Organization of the Fugu rubripes Hox clusters: evidence for  
 continuing evolution of vertebrate Hox complexes."  
 RL Nat. Genet. 16:79-83(1997).  
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).  
 DR EMBL: U92572; AAB68682.1; -  
 DR HSSP: P02833; 9ANT.  
 DR PROSITE: PS00027; HOMEBOX\_1; 1.  
 DR PRAM: PF00046; homeobox; 1.  
 DR PRINTS: PR00024; HOMEBOX.  
 DR PRINTS: PR00025; ANTENNAPEDIA.  
 KW Homeobox; DNA-binding; Nuclear  
 SQ SEQUENCE 236 AA; 27181 MW; 77DC03C CRC32;

Query Match 41.8%; Score 61; DB 13; Length 236;  
 Best Local Similarity 54.5%; Pred. No. 7.28e+00;  
 Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Db 76 FLODKDVLSPC 86  
 : 111:111:  
 QY 6 FLIATDLPAC 16

RESULT 14  
 ID 047099 PRELIMINARY; PRT; 254 AA.  
 AC 047099;  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last annotation update)  
 DE CS31A MINOR SUBUNIT PRECURSOR.  
 GN CLPL.  
 OS Escherichia coli.  
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
 OC Escherichia.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-K-12;  
 RA DER VARTANIAN M.;  
 RL Submitted (SEP-1993) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: L05182; AAA23586.1; -  
 KW signal.  
 FT SIGNAL 1 20 POTENTIAL.  
 FT CHAIN 21 254 CS31A MINOR SUBUNIT.  
 SQ SEQUENCE 254 AA; 27021 MW; 6B28C6FD CRC32;

Wed Mar 8 07:51:07 2000

Query Match	41.8%;	Score 61;	DB 2;	Length 254;
Best Local Similarity	63.6%;	Pred. No. 7.28e+00;		
Matches	7;	Conservative	2;	Mismatches 2; Indels 0; Gaps 0;

```
Db 7 ELFAASLLPSC 17
    |||: |||:|
Qy 6 FLHATDLLPAC 16
```

RESULT	15	PRELIMINARY;	PRT;	286 AA.
AC	Q41661;			
AC	Q41661;			
DT	01-NOV-1996 (TrEMBLrel. 01, Created)			
DT	01-NOV-1996 (TrEMBLrel. 01, Last sequence update)			
DT	01-NOV-1999 (TrEMBLrel. 12, Last annotation update)			
DE	POTATIVE NARBONIN-LIKE 2S PROTEIN.			
DE	vicia faba (Broad bean) .			
OC	Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta:			
OC	euphyllophytes: Spermatophyta: Magnoliophyta: eudicotyledons:			
OC	cure eudicotys: Rosidae: eurosids I, Fabales; Fabaceae; Papilionoideae:			
OC	vicia.			
OC	[1]			
RN	SEQUENCE FROM N.A.			
RP				
RC	TISSUE=COTYLEDON;			
RA	NONG V., SCHLESIER B., MUENTZ K.;			
RL	Submitted (NOV-1994) to the EMBL/Genbank/DBJ databases.			
DR	EMBL: J46834; CAAB6875.1; -			
DR	MENDL: 16614; Vicia:2552:16614.			
DR	PRINTS: PR00551; ZSGL0BL0ULN.			
Q3	SEQUENCE 286 AA: 32575 MW: ABE3A19D CRC32:			

Query Match	41.8%	Score 61;	DB 10;	Length 286;
Best Local Similarity	31.3%	Pred. No. 7.28e+00;		
Matches	5;	Conservative	6;	Mismatches 5; Indels 0; Gaps 0

```

Db      129 DINYEYIKSDELFVNC 144
        |::|:::|:|
Qy      1 DVNYAFLHATDLLPAC 16

```

Search completed: Tue Mar 7 21:07:26 2000  
Job time : 11 secs.

THIS PAGE BLANK (USPTO)



\*\*\*\*\*  
MUSE (TM)  
\*\*\*\*\*

Release 3.1A John F. Collins, Biocomputing Research Unit.  
Copyright (c) 1993-1998 University of Edinburgh, U.K.  
Distribution rights by Oxford Molecular Ltd

MPerch\_pp protein - protein database search, using Smith-Waterman algorithm  
Run on: Tue Mar 7 21:19:24 2000; Maspar time 3.17 Seconds  
149.639 Million cell updates/sec  
Tabular output not generated.

Title: >US-08-981-824-2  
Description: (1-20) from US08981824.pep  
Perfect Score: 159  
Sequence: 1 SNMYAMTARFKMPEVKEK 20

Scoring table: PAM 150  
Gap 15

Searched: 188963 seqs, 23686106 residues

Post-processing: Minimum Match 08  
Listing first 45 summaries

Database: a-geneseq35  
1:geneseqp

Statistics: Mean=20.912; Variance 73.027; scale 0.286

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	159	100.0	20	1	Human 65 kD glutamine	5.66e-09
2	159	100.0	20	1	W18843	5.66e-09
3	159	100.0	341	1	65 kD Glutamic acid de	5.66e-09
4	159	100.0	503	1	GAD65 1-244 N-terminal	5.66e-09
5	159	100.0	540	1	Human GAD65 gene produ	5.66e-09
6	159	100.0	540	1	GAD65 1-45 N-terminal	5.66e-09
7	159	100.0	544	1	GAD65 545-585 C-termin	5.66e-09
8	159	100.0	554	1	GAD65 1-31 deleted, C4	5.66e-09
9	159	100.0	584	1	Human GAD65 protein se	5.66e-09
10	159	100.0	584	1	Human GAD65 protein	5.66e-09
11	159	100.0	585	1	Human glutamic acid de	5.66e-09
12	159	100.0	585	1	Human pancreatic islet	5.66e-09
13	159	100.0	585	1	Human 65k-glutamic aci	5.66e-09
14	159	100.0	585	1	Human GAD 65.	5.66e-09
15	159	100.0	585	1	Human GAD65.	5.66e-09
16	159	100.0	585	1	65 kD human glutamic a	5.66e-09
17	155	97.5	20	1	Human GAD.	5.66e-09
18	148	93.1	341	1	Glutamic acid decarbox	1.57e-08
19	148	93.1	340	1	GAD65 1-244 N-terminal	9.32e-08
20	148	93.1	544	1	GAD65 1-45 N-terminal	9.32e-08
21	148	93.1	554	1	GAD65 545-585 C-termin	9.32e-08
22	148	93.1	584	1	GAD65 1-31 deleted, C4	9.32e-08
23	148	93.1	584	1	Rat GAD65 protein sequ	9.32e-08
					Rat GAD65 protein.	9.32e-08

24	148	93.1	585	1	R23644	Rat GAD65 gene product	9.32e-08
25	148	93.1	585	1	R59517	Rat GAD65.	9.32e-08
26	148	93.1	585	1	R29628	Rat GAD 65.	9.32e-08
27	148	93.1	594	1	W74717	Amino acid sequence of	9.32e-08
28	148	93.1	605	1	R71733	Rat glutamic acid deca	9.32e-08
29	147	92.5	585	1	W14916	Modified glutamic acid	1.20e-07
30	147	92.5	585	1	W14915	Modified glutamic acid	1.20e-07
31	126	79.2	20	1	W10300	Mammalian GAD 65 pepti	2.32e-05
32	122	76.7	14	1	W18861	65 kD Glutamic acid de	6.25e-05
33	122	76.7	14	1	R76653	Peptide derived from h	6.25e-05
34	121	76.1	23	1	R29627	GAD peptide.	8.00e-05
35	112	70.4	181	1	R27219	Islet GAD.	7.25e-04
36	112	70.4	593	1	R27220	Brain GAD #2.	7.25e-04
37	112	70.4	594	1	W74716	Amino acid sequence of	7.25e-04
38	112	70.4	594	1	R27221	Full length brain GAD.	7.25e-04
39	109	68.6	181	1	R27218	Brain GAD.	1.50e-03
40	103	64.8	594	1	R27222	Full length islet GAD.	6.38e-03
41	101	63.5	13	1	W35531	Glutamic acid decarbox	1.03e-02
42	91	57.2	506	1	W20064	Rat GADII protein.	1.10e-01
43	91	57.2	506	1	W22305	Rat GADII.	1.10e-01
44	87	54.7	493	1	W20065	Human GADII protein.	2.78e-01
45	87	54.7	493	1	W22306	Human GADII.	2.78e-01

## ALIGNMENTS

RESULT 1  
ID W01794 standard; peptide: 20 AA.  
AC W01794; (first entry)  
DT 15-OCT-1997  
DE Human 65 kD glutamine decarboxylase peptide.  
KW Human; glutamine decarboxylase; GAD; diagnosis; predisposition;  
KW tumour; immunological; disease; autoimmune; diabetes; reagent;  
KW determination; T cell; subpopulation; medication; treatment;  
KW prevention; production; antigen; immunogen; tolerogen; isolation;  
KW rejection; inactivation.  
OS Homo sapiens.  
PN DE19525784-A1.  
PD 16-JUN-1997.  
PF 14-JUL-1995; 025784.  
PR 14-JUL-1995; DE-025784.  
PA (BOER) BOEHRINGER MANNHEIM GMBH.  
PI Albert W, Boltaard C, Endl J, Jung G, Schendel D;  
PI Stahl P, Van Ender P;  
PI WPI: 97-078452/08.  
PT Glutamine decarboxylase peptide(s) - for diagnosis and therapy of  
PT diabetes, etc.  
PS Claim 1: Page 12; 15pp; German.  
CC The present peptide is a fragment of the human 65 kD glutamine  
CC decarboxylase (GAD), which can be used to diagnose, or diagnose a  
CC predisposition to, a tumour or immunological disease, preferably an  
CC autoimmune disease, especially diabetes. It can also be used as a  
CC reagent to determine specific T cell subpopulations, in medicaments  
CC to treat or prevent immunological diseases, preferably autoimmune  
CC diseases, especially diabetes, to produce antigens, especially  
CC immunogens or tolerogens and to isolate specific T cell  
CC subpopulations, which can be used to produce antigens or for  
CC reinjection, optionally after inactivation.  
SQ Sequence 20 AA:  
Query Match 100.0%; Score 159; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 5.66e-09;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
DB 1 SNMYAMTARFKMPEVKEK 20  
QY 1 SNMYAMTARFKMPEVKEK 20  
RESULT 2  
ID W18843 standard; peptide: 20 AA.  
AC W18843;  
DT 05-JAN-1998 (first entry)

DE 65 kD glutamic acid decarboxylase peptide fragment II.  
 KW GAD: 65 kD: human: glutamic acid decarboxylase; autoreactive; diagnosis;  
 KW insulin-dependent diabetes mellitus; IDDM; cell-mediated disease;  
 KW predisposition; autoimmune; tumour; rheumatoid arthritis;  
 KW multiple sclerosis.  
 OS Synthetic.  
 PN DE19526561-A1.  
 PD 23-JAN-1997.  
 PF 20-JUL-1995; 026561.  
 PR 20-JUL-1995; DE-026561.  
 PA (BOEF) BOEHRINGER MANNHEIM GMBH.  
 PI Donle F, Endl J, Ganz M, Jung G, Kientsch-engel R;  
 PI Pozzilli P, Stahl P;  
 DR WPI: 97-088254/09.  
 PT Skin test for diagnosis of cell-mediated diseases, esp. diabetes -  
 PT involving intradermal admn. of auto-reactive substances  
 PS Claim 11; Page 9; 12pp; German.  
 CC W18842-70 are peptide fragments of the 65 kD human glutamic acid  
 CC decarboxylase (GAD). The fragments are autoreactive substances used for  
 CC diagnosis of insulin-dependent diabetes mellitus (IDDM). The diagnosis is  
 CC determined by using a claimed method for diagnosis of cell-mediated  
 CC diseases or a predisposition to cell-mediated diseases, which is effected  
 CC by administering an autoreactive substance intradermally and establishing  
 CC the diagnosis on the basis of the occurrence or lack of a positive  
 CC reaction at the site of administration. The method is used for diagnosis  
 CC of autoimmune and tumour diseases, preferably T-cell-mediated diseases  
 CC such as rheumatoid arthritis, multiple sclerosis and especially IDDM.  
 SQ Sequence 20 AA;

Query Match 100.0%; Score 159; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 5.66e-09;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 SNMYAMMIARFKMPPEVKEK 20  
 OY 1 SNMYAMMIARFKMPPEVKEK 20

RESULT 3  
 ID R59522 standard; protein: 341 AA.  
 AC R59522;  
 DT 09-NOV-1994 (first entry)  
 DE GAD65 1-244 N-terminal-deleted mutant.  
 KW GAD65; glutamate-decarboxylase; diabetes mellitus;  
 KW stiff man syndrome; autoantibody; mutagenesis.  
 OS Homo sapiens.  
 PN W09412529-A.  
 PD 09-JUN-1994.  
 PF 02-DEC-1993; U11705.  
 PR 03-DEC-1992; US-984935.  
 PA (REGC) UNIV CALIFORNIA.  
 PI Baekkeskov S, Kim J, Nanchuk M, Richter W, Shi Y;  
 PI WPI: 94-200193/24.  
 PT New soluble fragments of glutamic acid decarboxylase protein -  
 PT used for the diagnosis and treatment of insulin dependent  
 PT diabetes mellitus and stiff man syndrome.  
 PS Disclosure; Fig. 1; 73pp; English.  
 CC The amino acid sequences of human GAD65 (R59516) and rat GAD65  
 CC (R59517) were determined. New soluble fragments of GAD65  
 CC (R59518-25) were prepared by deletion/substitution  
 CC mutagenesis. These fragments are free of N-terminal amino acids  
 CC that limit solubility. Different fragments contain epitopes for  
 CC different classes of GAD65 autoantibodies.  
 SQ Sequence 341 AA;

Query Match 100.0%; Score 159; DB 1; Length 341;  
 Best Local Similarity 100.0%; Pred. No. 5.66e-09;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 2 SNMYAMMIARFKMPPEVKEK 21  
 OY 1 SNMYAMMIARFKMPPEVKEK 20

RESULT 4  
 ID R23645 standard; Protein: 503 AA.  
 AC R23645;  
 DT 02-NOV-1992 (first entry)  
 DE Human GAD65 gene product.  
 KW Glutamic acid decarboxylase; IDDM; stiff man syndrome;  
 KW autoantibodies.  
 OS Homo sapiens.  
 PN W09205446-A.  
 PD 02-APR-1992.  
 PF 23-SEP-1991; 006872.  
 PR 21-SEP-1990; US-586536.  
 PA (REGC) UNIV CALIFORNIA.  
 PI Erlander MG, Kaufman DL, Tobin AJ;  
 DR WPI: 92-150489/18.  
 DR N-RSDB: 024184.  
 PT Novel cDNA encoding GAD65 polypeptide - used to produce GAD65 for  
 PT therapeutic and diagnostic application in insulin-dependent  
 PT diabetes mellitus patients  
 PS Disclosure; Fig 3; 53pp; English.  
 CC The sequence given is a glutamic acid decarboxylase (GAD65). GAD65  
 CC can be used for the diagnosis and therapy of patients with autoimmune  
 CC diseases, esp. insulin-dependant diabetes mellitus (IDDM) and "stiff  
 CC man" syndrome. It is possible to use either the entire GAD65 protein  
 CC or polypeptide fragments of it for the immunological detection of  
 CC autoantibodies to GAD65 which are indicative of IDDM and other auto-  
 CC immune diseases. The production of this sequence by recombinant DNA  
 CC technology allows large scale production of eukaryotic GAD65 in its  
 CC native form without the need for separation from other proteinaceous  
 CC prods.  
 SQ Sequence 503 AA;

Query Match 100.0%; Score 159; DB 1; Length 503;  
 Best Local Similarity 100.0%; Pred. No. 5.66e-09;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 246 SNMYAMMIARFKMPPEVKEK 265  
 OY 1 SNMYAMMIARFKMPPEVKEK 20

RESULT 5  
 ID R59520 standard; protein: 540 AA.  
 AC R59520;  
 DT 09-NOV-1994 (first entry)  
 DE GAD65 1-45 N-terminal-deleted mutant.  
 KW GAD65; glutamate-decarboxylase; diabetes mellitus;  
 KW stiff man syndrome; autoantibody; mutagenesis.  
 OS Homo sapiens.  
 PN W09412529-A.  
 PD 09-JUN-1994.  
 PF 02-DEC-1993; U11705.  
 PR 03-DEC-1992; US-984935.  
 PA (REGC) UNIV CALIFORNIA.  
 PI Baekkeskov S, Kim J, Nanchuk M, Richter W, Shi Y;  
 PI WPI: 94-200193/24.  
 PT New soluble fragments of glutamic acid decarboxylase protein -  
 PT used for the diagnosis and treatment of insulin dependent  
 PT diabetes mellitus and stiff man syndrome.  
 PS Disclosure; Fig. 1; 73pp; English.  
 CC The amino acid sequences of human GAD65 (R59516) and rat GAD65  
 CC (R59517) were determined. New soluble fragments of GAD65  
 CC (R59518-25) were prepared by deletion/substitution  
 CC mutagenesis. These fragments are free of N-terminal amino acids  
 CC that limit solubility. Different fragments contain epitopes for  
 CC different classes of GAD65 autoantibodies.  
 SQ Sequence 540 AA;

Query Match 100.0%; Score 159; DB 1; Length 540;  
 Best Local Similarity 100.0%; Pred. No. 5.66e-09;

Matches 20: Conservative 0: Mismatches 0: Indels 0: Gaps 0:  
Db 201 SNMYAMMIARFKMPEYKER 220  
|||||  
QY 1 SNMYAMMIARFKMPEYKER 20

RESULT 6  
ID R59524 standard: protein: 544 AA.

AC R59524;  
DT 09-NOV-1994 (first entry)  
DE GAD65 545-585 C-terminal-deleted mutant.  
KW GAD65; glutamate-decarboxylase; diabetes mellitus;  
stiff man syndrome; autoantibody; mutagenesis.  
OS Homo sapiens.  
PN MO9412529-A.  
PD 09-JUN-1994.  
PF 02-DEC-1993: U11705.  
PR 03-DEC-1992: US-984935.  
PS (REGC ) UNIV CALIFORNIA.  
PI Baekkeskov S, Kim J, Namchuk M, Richter W, Shi Y;  
DR WPI: 94-200193/24.  
PT New soluble fragments of glutamic acid decarboxylase protein -  
used for the diagnosis and treatment of insulin dependent  
PT diabetes mellitus and stiff man syndrome.  
PS Disclosure: Fig. 1; 73pp: English.  
CC The amino acid sequences of human GAD65 (R59516) and rat GAD65  
CC (R59517) were determined. New soluble fragments of GAD65  
CC (R59518-25) were prepared by deletion/substitution  
CC mutagenesis. The C-terminally deleted mutants given in R59524-25  
CC are able to recognize IDDM autoantibodies having the specificity  
CC of MICAA/MICAF, but not those having the specificity of MICAL/MICAF3  
CC or MICAA. These mutants also have some N-terminal modifications  
CC to improve solubility.  
SQ Sequence 544 AA;

Query Match 100.0%; Score 159; DB 1; Length 544;  
Best Local Similarity 100.0%; Pred. No. 5,66e-09;  
Matches 20: Conservative 0: Mismatches 0: Indels 0: Gaps 0;

Db 246 SNMYAMMIARFKMPEYKER 265  
|||||  
QY 1 SNMYAMMIARFKMPEYKER 20

RESULT 7  
ID R59518 standard: protein: 554 AA.  
AC R59518;  
DT 09-NOV-1994 (first entry)  
DE GAD65 1-31 deleted, C45A mutant.  
KW GAD65; glutamate-decarboxylase; diabetes mellitus;  
stiff man syndrome; autoantibody; mutagenesis.  
OS Homo sapiens.  
PN MO9412529-A.  
PD 09-JUN-1994.  
PF 02-DEC-1993: U11705.  
PR 03-DEC-1992: US-984935.  
PS (REGC ) UNIV CALIFORNIA.  
PI Baekkeskov S, Kim J, Namchuk M, Richter W, Shi Y;  
DR WPI: 94-200193/24.  
PT New soluble fragments of glutamic acid decarboxylase protein -  
used for the diagnosis and treatment of insulin dependent  
PT diabetes mellitus and stiff man syndrome.  
PS Disclosure: Fig. 1; 73pp: English.  
CC The amino acid sequences of human GAD65 (R59516) and rat GAD65  
CC (R59517) were determined. New soluble fragments of GAD65  
CC (R59518-25) were prepared by deletion/substitution  
CC mutagenesis. These fragments are free of N-terminal amino acids  
CC that limit solubility. Different fragments contain epitopes for  
CC different classes of GAD65 autoantibodies.  
SQ Sequence 554 AA;

Query Match 100.0%; Score 159; DB 1; Length 554;

Best Local Similarity 100.0%; Pred. No. 5,66e-09;  
Matches 20: Conservative 0: Mismatches 0: Indels 0: Gaps 0:  
Db 215 SNMYAMMIARFKMPEYKER 234  
|||||  
QY 1 SNMYAMMIARFKMPEYKER 20

RESULT 8  
ID W86017 standard: protein: 584 AA.

AC W86017;  
DT 22-FEB-1999 (first entry)  
DE Human GAD65 protein sequence.  
KW GAD65; autoantibody; soluble; detection; diagnosis; monitor; IDDM;  
insulin-dependent diabetes mellitus; stiff man syndrome.  
OS Homo sapiens.  
PN US5849506-A.  
PD 15-DEC-1998.  
PF 25-MAY-1995: 450755.  
PR 02-DEC-1993: US-161290.  
PR 03-DEC-1992: US-984935.  
PS (REGC ) UNIV CALIFORNIA.  
PI Baekkeskov S, Kim J, Namchuk M, Richter W, Shi Y;  
DR WPI: 99-069720/06.  
PT Immunoassay for GAD65 auto-antibodies - used for diagnosis of  
PT diabetes and stiff man syndrome  
PS Examples: Fig 1; 31pp: English.  
CC This represents a human GAD65 protein sequence. The invention provides  
CC soluble fragments of GAD65 that are specifically reactive with at least  
CC one class of GAD65 autoantibody. The fragments are substantially free of  
CC C-terminal amino acids that would otherwise limit solubility. Different  
CC fragments contain different epitopes for different classes of GAD65  
CC autoantibodies. These fragments are used in the methods of the invention  
CC for detection of GAD65 autoantibodies. The methods are used for  
CC diagnosing or monitoring insulin-dependent diabetes mellitus (IDDM) and  
CC stiff man syndrome.  
SQ Sequence 584 AA;

Query Match 100.0%; Score 159; DB 1; Length 584;  
Best Local Similarity 100.0%; Pred. No. 5,66e-09;  
Matches 20: Conservative 0: Mismatches 0: Indels 0: Gaps 0;

Db 246 SNMYAMMIARFKMPEYKER 265  
|||||  
QY 1 SNMYAMMIARFKMPEYKER 20

RESULT 9  
ID W34519 standard: protein: 584 AA.  
AC W34519;  
DT 24-MAR-1998 (first entry)  
DE Human GAD65 protein.  
KW GAD65; glutamic acid decarboxylase protein; human; soluble fragment;  
autoantibody; insulin-dependent diabetes mellitus; IDDM; diagnosis;  
stiff man syndrome; therapy.  
OS Homo sapiens.  
PN US5691448-A.  
PD 25-NOV-1997.  
PF 02-DEC-1993: 161290.  
PR 02-DEC-1993: US-161290.  
PR 03-DEC-1992: US-984935.  
PS (BAEK/) BAEKESKOV S.  
PA (KIM/) KIM J.  
PA (NAMC/) NAMCHUK M.  
PA (RICH/) RICHTER W.  
PI Baekkeskov S, Kim J, Namchuk M, Richter W, Shi Y;  
DR WPI: 98-017711/02.  
PT Soluble fragments of glutamic acid decarboxylase GAD65 - used to  
PT distinguish between insulin-dependent diabetes mellitus and  
PT stiff-man syndrome  
PS Disclosure: column 27-30; 30pp: English.

CC This sequence represents the human glutamic acid decarboxylase protein  
 CC GAD65. The invention relates to soluble fragments of a GAD65 protein that  
 CC are specifically reactive with a GAD65 autoantibody (Ab), where the  
 CC fragment is at least 98% pure and the Ab binds to a conformational  
 CC epitope of the fragment. The soluble GAD65 fragments can be used to  
 CC distinguish between insulin-dependent diabetes mellitus (IDDM) and stiff  
 CC man syndrome. They can also be used for diagnosis and treatment of IDDM  
 CC and stiff man syndrome. The fragments can distinguish different temporal  
 CC stages in the progression of IDDM.  
 SQ Sequence 584 AA;

Query Match 100.0%; Score 159; DB 1; Length 584;  
 Best Local Similarity 100.0%; Pred. No. 5,66e-09;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 246 SNMYAMTARFKMPPEVKEK 265  
 OY 1 SNMYAMTARFKMPPEVKEK 20

RESULT 10  
 ID R79105 standard; Protein; 585 AA.  
 AC R79105:  
 DT 13-NOV-1995 (first entry)  
 DE Human glutamic acid decarboxylase (GAD65).  
 KW Rat glutamic acid decarboxylase; GAD65; autoimmune disorders;  
 KW insulin-dependent diabetes mellitus; stiff man disease.  
 OS Homo sapiens.  
 PN W09507992-A.  
 PD 23-MAR-1995.  
 PF 24-AUG-1984; U09478.  
 PR 17-SEP-1993; US-123859.  
 PA (REGC ) UNIV CALIFORNIA.  
 PI Cläre-Salzler MJ, Erlander MG, Kaufman DL, Tobin AJ;  
 DR WPI: 95-131360/17.  
 DR N-PSDB: 086482.  
 PT New polypeptide fragments of glutamic acid decarboxylase - for  
 PT diagnosis and treatment of autoimmune disease, esp. insulin  
 PT dependent diabetes, also related nucleic acid, vectors,  
 PT antibodies, hybridoma(s) etc.  
 PS Example 1; Fig 3; 100pp; English.  
 CC 086481 and 086482 encode R71733 and R79105, rat and human glutamic  
 CC acid decarboxylase (GAD65) respectively, from which the GAD65  
 CC fragments described in R72261-R72298 were derived. These fragments  
 CC can be used to detect autoantibodies against GAD, e.g. to diagnose  
 CC and treat GAD-related autoimmune disorders, such as insulin  
 CC dependent diabetes mellitus or stiff man disease.  
 SQ Sequence 585 AA;

Query Match 100.0%; Score 159; DB 1; Length 585;  
 Best Local Similarity 100.0%; Pred. No. 5,66e-09;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 246 SNMYAMTARFKMPPEVKEK 265  
 OY 1 SNMYAMTARFKMPPEVKEK 20

RESULT 11  
 ID R28756 standard; Protein; 585 AA.  
 AC R28756:  
 DT 20-APR-1993 (first entry)  
 DE Human pancreatic islet cell glutamic acid decarboxylase.  
 KW GAD; insulin dependent diabetes melting; IDDM; autoantibody detection.  
 OS Homo sapiens.  
 PN W09220811-A.  
 PD 26-NOV-1992.  
 PR 14-MAY-1992; U04079.  
 PR 15-MAY-1991; US-702162.  
 PA (UNIM ) UNIV WASHINGTON.  
 PA (ZYMO ) ZYMOGENETICS INC.  
 PI Foster DC, Grubir CE, Hagopian W, Karlsten AE, Lermarck A, Ohara PJ;  
 DR WPI: 92-415789/50.

DR N-PSDB: Q31783.  
 PT Polynucleotide encoding human islet glutamic acid decarboxylase -  
 PT used to test for auto-antibodies against itself to diagnose  
 PT insulin dependent diabetes mellitus  
 PS Disclosure: Fig 2; 45pp; English.

CC The sequence is that of human pancreatic islet glutamic acid  
 CC decarboxylase (GAD) which is used to test biological samples for  
 CC the presence of autoantibodies to human GAD. It can also be used  
 CC to remove antibodies against GAD from plasma in order to treat an  
 CC autoimmune response to GAD, e.g. in insulin-dependent diabetes melting  
 CC (IDDM), and may also be used to induce immunological tolerance to GAD  
 CC by giving GAD that specifically binds the GAD receptor on immature T  
 CC or B cells.  
 SQ Sequence 585 AA;

Query Match 100.0%; Score 159; DB 1; Length 585;  
 Best Local Similarity 100.0%; Pred. No. 5,66e-09;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 246 SNMYAMTARFKMPPEVKEK 265  
 OY 1 SNMYAMTARFKMPPEVKEK 20

RESULT 12  
 ID W35361 standard; Protein; 585 AA.  
 AC W35361:  
 DT 22-APR-1998 (first entry)  
 DE Human 65K-glutamic acid decarboxylase.  
 KW Mouse; human; glutamic acid decarboxylase; GAD65; diagnosis;  
 KW autoimmune reaction; T cell; mammalian skin; autoimmune disease;  
 KW insulin independent diabetes; inflammation.  
 OS Homo sapiens.  
 PN W09736618-A1.  
 PD 09-OCT-1997.  
 PR 31-MAR-1997; J01104.  
 PR 01-APR-1996; JP-078878.  
 PA (CHUS ) CHUGAI SEIYAKU KK.  
 PI Kure S, Muto Y, Narisawa K, Sakata Y, Satoh J;  
 DR WPI: 97-502847/46.  
 PT Composition containing 65K-glutamic acid decarboxylase or its  
 PT partial peptide(s) - for diagnosing diseases associated with  
 PT auto-immune reaction  
 PS Claim 8; Page 14-16; 32pp; Japanese.  
 CC A composition has been developed for diagnosing diseases associated  
 CC with autoimmune reaction caused by 65K-glutamic acid decarboxylase  
 CC (GAD65) or its partial peptides. The composition reacts with T cells  
 CC in and/or on the surface of mammalian skin to cause inflammation.  
 CC The present sequence represents human GAD65. GAD65 and its partial  
 CC peptides are used to diagnose diseases associated with autoimmune  
 CC disease, e.g. insulin independent diabetes. The test is a very  
 CC simple skin test.  
 SQ Sequence 585 AA;

Query Match 100.0%; Score 159; DB 1; Length 585;  
 Best Local Similarity 100.0%; Pred. No. 5,66e-09;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 246 SNMYAMTARFKMPPEVKEK 265  
 OY 1 SNMYAMTARFKMPPEVKEK 20

RESULT 13  
 ID R29629 standard; Protein; 585 AA.  
 AC R29629:  
 DT 05-MAY-1993 (first entry)  
 DE Human GAD 65.  
 KW Glutamic acid decarboxylase; auto immune disease; insulin dependent;  
 KW diabetes mellitus; drug screening; antibody; stiff man syndrome.  
 OS Homo sapiens.  
 PN EP-519469-A.  
 PD 23-DEC-1992.

PF 17-JUN-1992: 110308.  
 PR 18-JUN-1991: US-716909.  
 PA (REGC ) UNIV CALIFORNIA.  
 PI Claret-Salzier MJ, Erlander MG, Kaufman DL, Tobin AJ;  
 DR WPI; 92-425701/52.  
 N-PSDB: 032760.  
 PT Glutamic acid decarboxylase isolated polypeptide(s) - useful for  
 diagnosis and treatment of auto-immune diseases, e.g. insulin  
 dependent diabetes mellitus, drug screening and antibody prodn.  
 PS Disclosure: Fig 3; 35pp; English.  
 CC The DNA encoding glutamic acid decarboxylase (GAD 65) was obtd. by  
 CC standard recombinant DNA techniques. The protein, or fragments of  
 CC it, may be used for the detection of autoantibodies to GAD 65.  
 CC It can also be used for screening drugs such as those that alter  
 CC GAD function and for generation of antibodies which can be used to  
 CC detect GAD 65. Such methods can be used in the diagnosis and  
 CC therapy of autoimmune diseases such as insulin dependent diabetes  
 CC mellitus and "stiff man" syndrome. The protein can be used to bind  
 CC or block the continuance of an autoimmune response to GAD 65.  
 CC It may also be coupled to therapeutic agents and used immunothe-  
 CCapeutically. See also R39625-8.  
 SQ Sequence 585 AA;  
 Query Match 100.0%; Score 159; DB 1; Length 585;  
 Best Local Similarity 100.0%; Pred. No. 5.66e-09;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Db 246 SNMYAMMIARFKMPVEYK 265  
 OY 1 SNMYAMMIARFKMPVEYK 20  
 RESULT 14  
 ID R59516 standard; protein: 585 AA.  
 AC R59516:  
 DT 09-NOV-1994 (first entry)  
 DE Human GAD65  
 KW GAD65; glutamate-decarboxylase; diabetes mellitus;  
 OS Homo sapiens.  
 PN MO9412529-A.  
 PD 09-JUN-1994.  
 PF 02-DEC-1993; U11705  
 PR 03-DEC-1992; US-984935.  
 PA (REGC ) UNIV CALIFORNIA.  
 PI Baekkeskov S, Kim J, Nanchuk M, Richter W, Shi Y;  
 DR WPI; 94-200193/24.  
 PT New soluble fragments of glutamic acid decarboxylase protein -  
 PT used for the diagnosis and treatment of insulin dependent  
 PT diabetes mellitus and stiff man syndrome.  
 PS Disclosure: Fig. 1; 73pp; English.  
 CC The amino acid sequences of human GAD65 (R59516) and rat GAD65  
 CC (R59517) were determined. New soluble fragments of GAD65  
 CC (R59518-25) were prepared by deletion/substitution  
 CC mutagenesis. These fragments are free of N-terminal amino acids  
 CC that limit solubility. Different fragments contain epitopes for  
 CC different classes of GAD65 autoantibodies.  
 SQ Sequence 585 AA;  
 Query Match 100.0%; Score 159; DB 1; Length 585;  
 Best Local Similarity 100.0%; Pred. No. 5.66e-09;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Db 246 SNMYAMMIARFKMPVEYK 265  
 OY 1 SNMYAMMIARFKMPVEYK 20  
 RESULT 15  
 ID W12402 standard; Protein: 585 AA.  
 AC W12402:  
 DT 08-OCT-1997 (first entry)  
 DE 65 kD human glutamic acid decarboxylase isoform.

KW 65 kD glutamic acid decarboxylase; human; GAD65; enzyme: pancreas;  
 KW neuron; central nervous system; type I diabetes; autoimmune response;  
 KW T cell; therapy.  
 OS Homo sapiens.  
 PN MO9700891-A1.  
 PD 09-JAN-1997.  
 PF 24-JUN-1996; U10790.  
 PR 23-JUN-1995; US-494624.  
 PA (KENN-) KENNEDY INST RHEUMATOLOGY.  
 PA (NEUR-) NEUROCRINE BIOSCIENCES INC.  
 PA (SEAR-) ST BARTHOLOMEW'S HOSPITAL CENT CLINICAL.  
 PI Conlon PJ, Gaur A, Leslie RDG, Ling N, Londei M;  
 DR WPI; 97-087322/08.  
 N-PSDB: T61097.  
 PT New human glutamic acid decarboxylase peptide(s) - used for  
 PT treatment, diagnosis and determining predisposition to diabetes and  
 PT for ameliorating auto-immune responses.  
 PS Disclosure: Fig 1; 28pp; English.  
 CC This sequence represents the 65 kD isoform of human glutamic acid  
 CC decarboxylase (GAD65). GAD is an enzyme expressed in the beta cells of  
 CC the pancreas, and in neurons of the central nervous system. There are two  
 CC isoforms of GAD, a 67 kD isoform, and GAD65. Immunodominant regions of  
 CC GAD65 have been identified in Type I diabetic patients. Fragments of  
 CC GAD65, and analogues of the fragments, are used in the methods of the  
 CC invention. The methods are for detecting or treating diabetes or a  
 CC predisposition to diabetes. The peptides can also be used for  
 CC ameliorating an autoimmune response in a patient. Alteration of the  
 CC native peptides with selective changes of crucial residues can induce  
 CC unresponsiveness or change the responsiveness of antigen-specific  
 CC autoreactive T cells. The peptide analogues compete for binding to MHC  
 CC and do not cause proliferation of the corresponding native  
 CC peptide-specific T cells.  
 SQ Sequence 585 AA;  
 Query Match 100.0%; Score 159; DB 1; Length 585;  
 Best Local Similarity 100.0%; Pred. No. 5.66e-09;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Db 246 SNMYAMMIARFKMPVEYK 265  
 OY 1 SNMYAMMIARFKMPVEYK 20

Search completed: Tue Mar 7 21:19:29 2000.  
 Job time : 5 secs.

**THIS PAGE BLANK (USPTO)**

\*\*\*\*\*  
Release 3.1a John F. Collins, Biocomputing Research Unit.  
Copyright (c) 1993-1998 University of Edinburgh, U.K.  
Distribution rights by Oxford Molecular Ltd  
\*\*\*\*\*  
(TW)

MPsrch\_dp protein - protein database search, using Smith-Waterman algorithm  
Run on: Tue Mar 7 21:16:05 2000; MasPar time 5.48 Seconds  
Tabular output not generated. 172.132 Million cell updates/sec

Title: >US-08-981-824-2  
Description: (1-20) from US08981824.pep  
Perfect Score: 159  
Sequence: 1 SNMYAMTARFKMFPEVK 20

Scoring table: PAM 150  
Gap 15

Searched: 142080 seqs, 47172406 residues

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: pir62  
1:pir1 2:pir2 3:pir3 4:pir4

Statistics: Mean-30-041; Variance 49.478; scale 0.607

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	159	100.0	585	1 A41292	glutamate decarboxyla	4.75e-18
2	152	95.6	585	1 JC4064	glutamate decarboxyla	1.55e-16
3	148	93.1	205	2 I67412	65 kda glutamate deca	1.11e-15
4	148	93.1	585	1 JH0423	glutamate decarboxyla	1.11e-15
5	148	93.1	585	1 S38533	glutamate decarboxyla	1.11e-15
6	116	73.0	594	1 A46758	glutamate decarboxyla	4.89e-09
7	112	70.4	206	2 I53274	glutamate decarboxyla	3.06e-08
8	112	70.4	585	2 S61534	glutamate decarboxyla	3.06e-08
9	112	70.4	593	1 A41367	glutamate decarboxyla	3.06e-08
10	112	70.4	593	2 S48135	glutamate decarboxyla	3.06e-08
11	112	70.4	593	2 S51776	glutamate decarboxyla	3.06e-08
12	112	70.4	594	1 B41935	glutamate decarboxyla	3.06e-08
13	112	70.4	594	1 JC4065	glutamate decarboxyla	3.06e-08
14	112	70.4	594	2 S51775	glutamate decarboxyla	3.06e-08
15	91	57.2	493	2 S71489	sulfolipase decarbox	1.12e-04
16	88	55.3	510	1 A30999	glutamate decarboxyla	1.12e-03
17	74	46.3	470	2 F72238	conserved hypothetical	3.03e-01
18	72	45.3	191	2 D69867	hypothetical protein	6.45e-01
19	72	45.3	622	2 A34711	kinase-related protei	6.45e-01
20	72	45.3	622	2 I48733	protein kinase rck (E	6.45e-01
21	72	45.3	1608	2 T13216	minor capsid protein	9.38e-01
22	71	44.7	254	2 A66437	hypothetical protein	9.38e-01
23	68	42.8	329	2 F69849	probable heme A farne	2.83e+00

24	66	41.5	280	2 T04432	protein kinase homolo	5.81e+00
25	66	41.5	580	2 F64385	hypothetical protein	5.81e+00
26	65	40.9	47	2 H70254	hypothetical protein	8.28e+00
27	65	40.9	387	2 F69427	conserved hypothetical	8.28e+00
28	65	40.9	587	2 A49942	hypothetical protein	8.28e+00
29	65	40.9	1553	2 T03301	rbf3 effector protein	8.28e+00
30	64	40.3	303	2 B69160	mevalonate kinase - M	1.18e+01
31	64	40.3	417	2 S36389	protein kinase B (EC	1.18e+01
32	64	40.3	423	1 MRBY	mRNA maturase b13 - y	1.18e+01
33	64	40.3	453	2 S78662	mRNA maturase SCB12	1.18e+01
34	64	40.3	424	2 JC3445	protein kinase (EC 2.	1.18e+01
35	64	40.3	480	2 JC2437	Rac protein kinase al	1.18e+01
36	64	40.3	480	2 A39360	protein kinase (EC 2.	1.18e+01
37	64	40.3	480	1 S33364	serine/threonine-spec	1.18e+01
38	64	40.3	480	1 S62117	protein kinase B (EC	1.18e+01
39	64	40.3	763	1 A40831	gag-akt polypeptide -	1.18e+01
40	64	40.3	906	1 S32607	trifunctional enzyme	1.18e+01
41	64	40.3	1049	2 B36938	acetylcholinesterase	1.18e+01
42	64	40.3	3924	2 S37431	ankyrin 2, neuronal 1	1.18e+01
43	63	39.6	326	2 T15194	hypothetical protein	1.66e+01
44	63	39.6	513	1 S62452	probable protein kina	1.66e+01
45	63	39.6	729	2 B70333	hypothetical protein	1.66e+01

ALIGNMENTS

RESULT 1  
ENTRY A41292 #type complete  
TITLE glutamate decarboxylase (EC 4.1.1.15) 2 - human  
ALTERNATE\_NAMES glutamate decarboxylase GAD65; L-glutamate 1-carboxy-lyase  
ORGANISM Homo sapiens #common\_name man  
DATE 13-May-1992 #sequence\_revision 23-Mar-1995 #text\_change 18-Jun-1999  
ACCESSIONS A41935; A41292; S30058; B54778  
REFERENCE A41935  
#authors Bu, D.F.; Erlender, M.G.; Hitz, B.C.; Tillakaratne, N.J.K.; Kaufman, D.L.; Wagner-McPherson, C.B.; Evans, G.A.; Tobin, A.J.  
#journal Proc. Natl. Acad. Sci. U.S.A. (1992) 89:2115-2119  
#title Two human glutamate decarboxylases, 65-kDa GAD and 67-kDa GAD, are each encoded by a single gene.  
#cross-references MIM:92196068  
#accession A41935  
#molecule\_type mRNA  
#residues 1-585 #label BU1  
##cross-references GB:M81882; NID:G182933; PIDN:AA62367.1; PID:G182934  
##experimental\_source brain  
#note Sequence extracted from NCBI backbone (NCBIF:88007)  
REFERENCE A41292  
#authors Karlsson, A.E.; Hagopian, W.A.; Grublin, C.E.; Dube, S.; Distche, C.M.; Adler, D.A.; Baermeier, H.; Mathewes, S.; Grant, F.J.; Foster, D.; Lermack, A.  
#journal Proc. Natl. Acad. Sci. U.S.A. (1991) 88:8337-8341  
#title Cloning and primary structure of a human islet 10. glutamic acid decarboxylase from chromosome 10.  
#cross-references MIM:92020848  
#accession A41292  
#molecule\_type mRNA  
#residues 1-585 #label KAR  
##cross-references GB:M74826; NID:G182931; PIDN:AA58491.1; PID:G182932  
##experimental\_source pancreatic islet  
#note S30058  
REFERENCE S30058  
#authors Mauch, L.; Ahney, C.C.; Berg, H.; Scherbaum, W.A.; Liedvogel, B.; Northemann, W.  
#journal Eur. J. Biochem. (1993) 212:597-603  
#title Characterization of a linear epitope within the human pancreatic 64-kDa glutamic acid decarboxylase and its autoimmune recognition by sera from insulin-dependent diabetes mellitus patients.  
#cross-references MIM:93185681  
#accession S30058  
#molecule\_type mRNA  
#residues 6-585 #label MAU

```

#cross-references EMBL:X69936
#experimental_source pancreatic islet
REFERENCE
#authors Bu, D.F.; Tobin, A.J.
#journal Genomics (1994) 21:222-228
#title The exon-intron organization of the genes (GAD1 and GAD2) encoding two human glutamate decarboxylases (GAD-67 and GAD-65) suggests that they derive from a common ancestral GAD.

#cross-references M0ID:94375018
#contents annotation; intron-exon boundaries
COMMENT This enzyme (GAD) catalyzes the formation of an inhibitory neurotransmitter, gamma-aminobutyric acid, from L-glutamic acid; it has several isoforms, each encoded by a separate gene. GAD has also been implicated as an autoantigen in autoimmune disease stiff-man syndrome and insulin-dependent diabetes mellitus.

GENETICS
#gene GDB:GAD2
#cross-references GDB:128595; OMIM:138275
#map_position 10p11.23-10p11.23
CLASSIFICATION #superfamily human glutamate decarboxylase
KEYWORDS carbon-carbon lyase; carboxy-lyase; phosphoprotein; pyridoxal phosphate

FEATURE
396 #binding_site pyridoxal phosphate (Lys) (covalent)
SUMMARY #status predicted
#length 585 #molecular-weight 65411 #checksum 4799

Query Match
Best Local Similarity 100.0%; Score 159; DB 1; Length 585;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 246 SNNYAMLIARFKMFPEVK 265
OY 1 SNNYAMLIARFKMFPEVK 20

RESULT 2
ENTRY J04064 #type complete
TITLE glutamate decarboxylase (EC 4.1.1.15) 65K chain - pig
ORGANISM #formal_name Sus scrofa domestica #common_name domestic pig
DATE 30-Jun-1995 #sequence_revision 14-Jul-1995 #text_change 22-Jun-1999
J04064

ACCESSIONS
REFERENCE J04064
#authors Suzuki, R.; Asami, N.; Amann, E.; Wagatsuma, M.
#journal Gene (1995) 152:257-260
#title Sequences of two porcine glutamic acid decarboxylases (65-and 67-kDa GAD).
#cross-references M0ID:95137399
#accession J04064
#molecule_type mRNA
#residues 1-585 #label SUZ
#cross-references DDBJ:D31848; NID:9790964; PIDN:BA06635.1;
PID:d1007207; PID:g790965

COMMENT #experimental_source brain
#text This enzyme catalyzes the conversion of glutamic acid into gamma-amino butyric acid.
CLASSIFICATION #superfamily human glutamate decarboxylase
KEYWORDS carbon-carbon lyase; carboxy-lyase

FEATURE
393-396 #domain DOPA decarboxylase binding #status predicted
SUMMARY #length 585 #molecular-weight 65388 #checksum 5933
#label BIN

Query Match
Best Local Similarity 95.6%; Score 152; DB 2; Length 585;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 246 SNNYAMLIARFKMFPEVK 265
OY 1 SNNYAMLIARFKMFPEVK 20

```

```

RESULT 3
ENTRY I67412 #type fragment
TITLE 65 kDa glutamate decarboxylase, brain - mouse (fragment)
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 27-Feb-1997 #sequence_revision 27-Feb-1997 #text_change 30-May-1997
I67412

ACCESSIONS
REFERENCE I33274
#authors Faulkner-Jones, B.E.; Cram, D.S.; Kun, J.; Harrison, L.C.
#journal Endocrinology (1993) 133:2962-2972
#title Localization and quantitation of expression of two glutamate decarboxylase genes in pancreatic beta-cells and other peripheral tissues of mouse and rat.
#cross-references M0ID:94062679
#accession I67412
#status preliminary; translated from GB/EMBL/DDBJ
#molecule_type mRNA
#residues 1-205 #label RES
#cross-references GB:567454; NID:9456852
CLASSIFICATION #superfamily human glutamate decarboxylase
SUMMARY #length 205 #checksum 3167

Query Match
Best Local Similarity 93.1%; Score 148; DB 2; Length 205;
Matches 18; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 72 SNNYAMLIARFKMFPEVK 91
OY 1 SNNYAMLIARFKMFPEVK 20

RESULT 4
ENTRY JH0423 #type complete
TITLE glutamate decarboxylase (EC 4.1.1.15) 2 - rat
ALTERNATE_NAMES glutamate decarboxylase GAD65; L-glutamate 1-carboxy-lyase
ORGANISM #formal_name Rattus norvegicus #common_name Norway rat
DATE 31-Mar-1992 #sequence_revision 23-Mar-1995 #text_change 18-Jun-1999
JH0423; A60888

ACCESSIONS
REFERENCE JH0423
#authors Erlander, M.G.; Tillakaratne, N.J.K.; Feldblum, S.; Patel, N.; Tobin, A.J.
#journal Neuron (1991) 7:91-100
#title Two genes encode distinct glutamate decarboxylases.
#cross-references M0ID:91299343
#accession JH0423
#molecule_type mRNA
#residues 1-585 #label ERL
#cross-references GB:M72422; NID:g204225; PIDN:AAA63488.1; PID:g204226
#experimental_source brain
#note the authors translated the codon GAT for residue 86 as His, TCA for residue 198 as Ala, and CAG for residue 428 as Trp

REFERENCE
A60888
#authors Chang, Y.C.; Gottlieb, D.I.
#journal J. Neurosci. (1988) 8:2123-2130
#title Characterization of the proteins purified with monoclonal antibodies to glutamic acid decarboxylase.
#cross-references M0ID:88258610
#accession A60888
#status preliminary
#molecule_type protein
#residues 'V',191-194, 'X',196-203, 'XX',206-219, 'X',225-234, 'X',236-247, 'X',249-266, 'X',524-537,539-543, 'V',547-549, 'X',551-553, 'X',555-558 #label CHA

COMMENT This enzyme (GAD) catalyzes the formation of an inhibitory neurotransmitter, gamma-aminobutyric acid, from L-glutamic acid; it has several isoforms, each encoded by a separate gene.
CLASSIFICATION #superfamily human glutamate decarboxylase
KEYWORDS carbon-carbon lyase; carboxy-lyase; phosphoprotein; pyridoxal phosphate

FEATURE

```



396 #binding\_site pyridoxal phosphate (Lys) (covalent)  
#status predicted  
SUMMARY #length 585 #molecular-weight 65402 #checksum 7756

Query Match 93.1%; Score 148; DB 1; Length 585;  
Best Local Similarity 90.0%; Pred. No. 1,11e-15;  
Matches 18; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 246 SNMYAMLIARKKPEVKEK 265  
|||||:|||||  
QY 1 SNMYAMLIARKKPEVKEK 20

RESULT 5  
ENTRY S38533 #type complete  
TITLE glutamate decarboxylase (EC 4.1.1.15) 2 - mouse  
ALTERNATE\_NAMES glutamate decarboxylase GAD65; L-glutamate 1-carboxy-lyase  
ORGANISM #formal\_name Mus musculus #common\_name house mouse  
DATE 20-May-1994 #sequence\_revision 23-Mar-1995 #text\_change 18-Jun-1999

ACCESSIONS S38533  
REFERENCE S38533  
#authors Lee, D.S.; Tian, J.; Phan, T.; Kaufman, D.L.  
#journal Biochim. Biophys. Acta (1993) 1216:157-160  
#title Cloning and sequence analysis of a murine cDNA encoding glutamate decarboxylase (GAD65).

#cross-references M0ID:94032481  
#accession S38533  
#status preliminary  
#molecule\_type mRNA  
#residues 1-585 #label LEE  
COMMENT #cross-references GB:L16980; NID:g413867; PIDN:AAA93049.1; PID:g413868  
This enzyme (GAD) catalyzes the formation of an inhibitory neurotransmitter, gamma-aminobutyric acid, from L-glutamic acid; it has several isoforms, each encoded by a separate gene.

CLASSIFICATION #superfamily human glutamate decarboxylase  
KEYWORDS carbon-carbon lyase; carboxy-lyase; phosphoprotein; pyridoxal phosphate

FEATURE 396  
#binding\_site pyridoxal phosphate (Lys) (covalent)  
#status predicted  
SUMMARY #length 585 #molecular-weight 65224 #checksum 7599

Query Match 93.1%; Score 148; DB 1; Length 585;  
Best Local Similarity 90.0%; Pred. No. 1,11e-15;  
Matches 18; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 246 SNMYAMLIARKKPEVKEK 265  
|||||:|||||  
QY 1 SNMYAMLIARKKPEVKEK 20

RESULT 6  
ENTRY A46758 #type complete  
TITLE glutamate decarboxylase (EC 4.1.1.15) 1 - cat  
ALTERNATE\_NAMES glutamate decarboxylase GAD67; L-glutamate 1-carboxy-lyase  
ORGANISM #formal\_name Felis silvestris catus #common\_name domestic cat  
DATE 31-Dec-1993 #sequence\_revision 23-Mar-1995 #text\_change 18-Jun-1999

ACCESSIONS A46758; A45671  
REFERENCE A46758  
#authors Kobayashi, Y.; Kaufman, D.L.; Tobin, A.J.  
#submission submitted to GenBank, September 1989  
#accession A46758  
#molecule\_type mRNA  
#residues 1-594 #label KOB  
#cross-references GB:M18629; NID:g163858; PIDN:AAA51430.1; PID:g163859

REFERENCE A45671  
#authors Kobayashi, Y.; Kaufman, D.L.; Tobin, A.J.  
#journal J. Neurosci. (1987) 7:2768-2772  
#title Glutamic acid decarboxylase cDNA: nucleotide sequence encoding an enzymatically active fusion protein.  
#cross-references M0ID:87310623

#accession A45671  
#molecule\_type mRNA  
#residues 1-558, RGRPRFGWSSRRQLHSPIITSSSR; #label K02  
#note this sequence has been revised in reference A46758  
COMMENT This enzyme (GAD) catalyzes the formation of an inhibitory neurotransmitter, gamma-aminobutyric acid, from L-glutamic acid; it has several isoforms, each encoded by a separate gene.

GENETICS  
#gene GAD1  
CLASSIFICATION #superfamily human glutamate decarboxylase  
KEYWORDS carbon-carbon lyase; carboxy-lyase; phosphoprotein; pyridoxal phosphate

FEATURE 405  
#binding\_site pyridoxal phosphate (Lys) (covalent)  
#status predicted  
SUMMARY #length 594 #molecular-weight 66824 #checksum 5630

Query Match 73.0%; Score 116; DB 1; Length 594;  
Best Local Similarity 70.0%; Pred. No. 4.89e-09;  
Matches 14; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Db 255 SNMYSIMAARKKPEVKT 274  
|||||:|||||  
QY 1 SNMYSIMAARKKPEVKT 20

RESULT 7  
ENTRY I53274 #type fragment  
TITLE glutamate decarboxylase, 67K, brain - mouse (fragment)  
ORGANISM #formal\_name Mus sp. #common\_name mouse  
DATE 12-Aug-1996 #sequence\_revision 12-Aug-1996 #text\_change 16-Feb-1997

ACCESSIONS I53274  
REFERENCE I53274  
#authors Faulkner-Jones, B.E.; Cram, D.S.; Kun, J.; Harrison, L.C.  
#journal Endocrinology (1993) 133:2962-2972  
#title Localization and quantitation of expression of two glutamate decarboxylase genes in pancreatic beta-cells and other peripheral tissues of mouse and rat.

#cross-references M0ID:94062679  
#accession I53274  
#status preliminary; translated from GB/EMBL/DBJ  
#molecule\_type mRNA  
#residues 1-206 #label RES  
#cross-references GB:S67453; NID:g456853  
CLASSIFICATION #superfamily human glutamate decarboxylase  
SUMMARY #length 206 #checksum 3323

Query Match 70.4%; Score 112; DB 2; Length 206;  
Best Local Similarity 70.0%; Pred. No. 3.05e-08;  
Matches 14; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Db 57 SNMYSIMAARKKPEVKT 76  
|||||:|||||  
QY 1 SNMYSIMAARKKPEVKT 20

RESULT 8  
ENTRY S61534 #type complete  
TITLE glutamate decarboxylase (EC 4.1.1.15) 62K isoform - mouse  
ALTERNATE\_NAMES glutamic acid decarboxylase  
ORGANISM #formal\_name Mus musculus #common\_name house mouse  
DATE 19-Mar-1997 #sequence\_revision 25-Apr-1997 #text\_change 22-Jun-1999

ACCESSIONS S61534; S61533  
REFERENCE S61534  
#authors Katarova, Z.; Szabo, G.; Mugnai, E.; Greenspan, R.J.  
#journal Eur. J. Neurosci. (1990) 2:190-202  
#title Molecular identification of the 62 kd form of glutamic acid decarboxylase from the mouse.  
#accession S61534  
#molecule\_type mRNA  
#residues 1-585 #label KAT

```
##cross-references EMBL:249976
##experimental_source brain
REFERENCE
#authors Szabo, G.
#submission submitted to the EMBL Data Library, June 1995
#accession S61533
#molecule_type mRNA
#residues 1-554, 'YQPGDKANFRWVSNPAASQSDIDFLTEIRLGODL' ##label
SZA
##cross-references EMBL:249976; NID:g886686; PIDN:CAA90277.1;
PID:g886687
##experimental_source brain
#note the differences at the carboxyl end are due to a
frameshift error
CLASSIFICATION #superfamily human glutamate decarboxylase
KEYWORDS carbon-carbon lyase; carboxy-lyase
SUMMARY #length 585 #molecular-weight 65381 #checksum 5716

Query Match 70.4%; Score 112; DB 2; Length 585;
Best Local Similarity 70.0%; Pred. No. 3.06e-08;
Matches 14; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

DB 254 SNMYTMMARKYKPEVVK 273
||||:| | | | | | |
Oy 1 SNMYTMMARKYKPEVVK 20

RESULT 9
ENTRY A41367 #type complete
TITLE glutamate decarboxylase (EC 4.1.1.15) 1 - rat
ALTERNATE_NAMES glutamate decarboxylase GAD67; L-glutamate 1-carboxy-lyase
ORGANISM #formal_name Rattus norvegicus #common_name Norway rat
DATE 12-Jun-1992 #sequence_revision 23-Mar-1995 #text_change
18-Jun-1999
ACCESSIONS A41367; A43756; JH0195
REFERENCE A41367
#authors Michelsen, B.K.; Petersen, J.S.; Boel, E.; Moldrup, A.;
Dyberg, T.; Madsen, O.D.
#journal Proc. Natl. Acad. Sci. U.S.A. (1991) 88:8754-8758
#title Cloning, characterization, and autoimmune recognition of rat
islet glutamic acid decarboxylase in insulin-dependent
diabetes mellitus.
#cross-references MUID:92020930
#accession A41367
#status preliminary
#molecule_type mRNA
#residues 1-593 ##label MIC
REFERENCE ##cross-references GB:M76177; NID:g704227; PIDN:AAA4184.1; PID:g704228
A43756
#authors Wyborski, R.J.; Bond, R.W.; Gottlieb, D.I.
#journal Brain Res. Mol. Brain Res. (1990) 8:193-198
#title Characterization of a cDNA coding for rat glutamic acid
decarboxylase.
#cross-references MUID:91014554
#accession A43756
#status preliminary
#molecule_type mRNA
#residues 1-593 ##label WVB
##cross-references GB:X57573; NID:g56183; PIDN:CAA4080.1; PID:g56184
#note the authors translated the codon TGT for residue 412 as
Ser and TCT for residue 413 as Cys
REFERENCE JH0195
#authors Julien, J.F.; Samama, P.; Maillet, J.
#journal J. Neurochem. (1990) 54:703-705
#title Rat brain glutamic acid decarboxylase sequence deduced from a
cloned cDNA.
#cross-references MUID:90132703
#accession JH0195
#molecule_type mRNA
#residues 1-102, 'V', '104-283', 'S', '285-286', 'AD', '289-343', 'EA', '346', 'I',
'348-351', 'LE', '354-379', 'R', '381-593' ##label JUL
##cross-references GB:X57572; NID:g56185; PIDN:CAA4080.1; PID:g56186
COMMENT This enzyme (GAD) catalyzes the formation of an inhibitory
```

```
neurotransmitter, gamma-aminobutyric acid, from L-glutamic acid;
it has several isoforms, each encoded by a separate gene.
CLASSIFICATION #superfamily human glutamate decarboxylase
KEYWORDS carbon-carbon lyase; carboxy-lyase; phosphoprotein; pyridoxal
phosphate
FEATURE
404 #binding_site pyridoxal phosphate (lys) (covalent)
SUMMARY #status predicted
#length 593 #molecular-weight 66640 #checksum 3971

Query Match 70.4%; Score 112; DB 1; Length 593;
Best Local Similarity 70.0%; Pred. No. 3.06e-08;
Matches 14; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

DB 254 SNMYTMMARKYKPEVVK 273
||||:| | | | | | |
Oy 1 SNMYTMMARKYKPEVVK 20

RESULT 10
ENTRY S48135 #type complete
TITLE glutamate decarboxylase (EC 4.1.1.15) - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 14-Jul-1995 #sequence_revision 10-Nov-1995 #text_change
07-May-1999
ACCESSIONS S48135
REFERENCE S48135
#authors Kelly, C.D.; Edwards, Y.; Johnstone, A.P.; Harfst, E.;
Nogradi, A.; Nussey, S.S.; Povey, S.; Carter, N.D.
#journal Ann. Hum. Genet. (1992) 56:255-265
#title Nucleotide sequence and chromosomal assignment of a cDNA
encoding the large isoform of human glutamate
decarboxylase.
#cross-references MUID:93080286
#accession S48135
#molecule_type mRNA
#residues 1-593 ##label KEL
##cross-references EMBL:222750
CLASSIFICATION #superfamily human glutamate decarboxylase
KEYWORDS carbon-carbon lyase; carboxy-lyase
SUMMARY #length 593 #molecular-weight 66952 #checksum 4836

Query Match 70.4%; Score 112; DB 2; Length 593;
Best Local Similarity 70.0%; Pred. No. 3.06e-08;
Matches 14; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

DB 254 SNMYTMMARKYKPEVVK 273
||||:| | | | | | |
Oy 1 SNMYTMMARKYKPEVVK 20

RESULT 11
ENTRY S51776 #type complete
TITLE glutamate decarboxylase (EC 4.1.1.15) - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 15-Jul-1995 #sequence_revision 21-Jul-1995 #text_change
16-Feb-1997
ACCESSIONS S51776
REFERENCE S51775
#authors Johnstone, A.
#submission submitted to the EMBL Data Library, May 1993
#accession S51776
#status preliminary
#molecule_type mRNA
#residues 1-593 ##label JOH
##cross-references EMBL:222750
#note this is an unpublished revision to the sequence from
reference S48135
CLASSIFICATION #superfamily human glutamate decarboxylase
KEYWORDS carbon-carbon lyase; carboxy-lyase
SUMMARY #length 593 #molecular-weight 66946 #checksum 4842

Query Match 70.4%; Score 112; DB 2; Length 593;
```

Best Local Similarity 70.0%; Pred. No. 3.06e-08;  
Matches 14; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Db 254 SNMYSIMAAKYKPEVKTR 273  
||||:|||||  
QY 1 SNMYSIMAAIRFKMPEVKKEK 20

RESULT 12  
ENTRY B41935 #type complete  
TITLE glutamate decarboxylase (EC 4.1.1.15) 1 - human  
ALTERNATE\_NAMES glutamate decarboxylase GAD67; L-glutamate 1-carboxy-lyase  
ORGANISM #formal\_name Homo sapiens #common\_name man  
DATE 31-Dec-1993 #sequence\_revision 23-Mar-1995 #text\_change 18-Jun-1999  
ACCESSION B41935; JH0805; JH0806; A61406; PQ0157; PQ0158; B41367;  
A36463; A54778  
REFERENCE A41935  
#authors Bu, D.F.; Erlander, M.G.; Hitz, B.C.; Tiliakaratne, N.J.K.;  
Kautman, D.L.; Wagner-McPherson, C.B.; Evans, G.A.; Tobin,  
A.J.  
#journal Proc. Natl. Acad. Sci. U.S.A. (1992) 89:2115-2119  
#title Two human glutamate decarboxylases, 65-kDa GAD and 67-kDa  
GAD, are each encoded by a single gene.  
#cross-references MUID:92196068  
#accession B41935  
#molecule\_type mRNA  
#residues 1-594 ##label BU1  
#cross-references GB:M81883; NID:g182935; PIDN:AAA62368.1; PID:g182936  
##experimental\_source pancreatic islet  
##note Sequence extracted from NCBI backbone (NCBIP:88006)

REFERENCE JH0805  
#authors Kawasaki, E.; Moriyuchi, R.; Watanabe, M.; Saitoh, K.; Charles  
Brunicardi, F.; Watt, P.C.; Yamaguchi, T.; Mullen, Y.;  
Akazawa, S.; Miyamoto, T.; Nagataki, S.  
#journal Biochem. Biophys. Res. Commun. (1993) 192:1353-1359  
#title Cloning and expression of large isoform of glutamic acid  
decarboxylase from human pancreatic islet.  
#cross-references MUID:93282845  
#accession JH0805  
##molecule\_type mRNA  
##residues 1-17,'N',19-30,'N',32-67,'K',68-115,'L',117-154,'T',  
156-301,'C',303,476,'G',478-991,'G',493-594 ##label  
KAW  
#cross-references GB:561898; NID:g385310; PIDN:AAB26938.1; PID:g385311  
##experimental\_source pancreatic islet

REFERENCE JH0806  
#authors Yamashita, K.; Cram, D.S.; Harrison, L.C.  
#journal Biochem. Biophys. Res. Commun. (1993) 192:1347-1352  
#title Molecular cloning of full-length glutamic acid decarboxylase  
67 from human pancreas and islets.  
#cross-references MUID:93282844  
#accession JH0806  
##molecule\_type mRNA  
##residues 1-67,'K',68-435,'L',437-511,'S',513-594 ##label YAM  
#cross-references GB:561897; NID:g385450; PIDN:AAB26937.1; PID:g385451  
##experimental\_source pancreatic islet

REFERENCE A61406  
#authors Kelly, C.; Carter, N.D.; Johnstone, A.P.; Nussey, S.S.  
#journal Lancet (1991) 338:1468-1469  
#title Cloning of large isoform of human brain glutamic acid  
decarboxylase.  
#cross-references MUID:92065769  
#accession A61406  
##molecule\_type mRNA  
##residues 62-67,'K',69-205,'N',207-564,'L',566-594 ##label KEL  
##experimental\_source brain

REFERENCE PQ0157  
#authors Cram, D.S.; Barnett, L.D.; Joseph, J.L.; Harrison, L.C.  
#journal Biochem. Biophys. Res. Commun. (1991) 176:1239-1244  
#title Cloning and partial nucleotide sequence of human glutamic  
acid decarboxylase cDNA from brain and pancreatic islets.  
#cross-references MUID:91248209

#accession PQ0157  
##molecule\_type mRNA  
##residues 218-463 ##label CRI  
#cross-references GB:M70434  
##experimental\_source brain  
#accession PQ0158  
##molecule\_type mRNA  
##residues 218-234,'K',236-240,'N',242-288,'H',290-323,'L',325-329,  
'D',331-338,'L',340-390,'S',392-397 ##label CR2  
#cross-references GB:M70435; NID:g182941; PIDN:AAA52513.1; PID:g182942  
##experimental\_source pancreatic islet

REFERENCE A41367  
#authors Michelsen, B.K.; Petersen, J.S.; Boel, E.; Moldrup, A.;  
Dyberg, T.; Madsen, O.D.  
#journal Proc. Natl. Acad. Sci. U.S.A. (1991) 88:8754-8758  
#title Cloning, characterization, and autoimmune recognition of rat  
islet glutamic acid decarboxylase in insulin-dependent  
diabetes mellitus.  
#cross-references MUID:92020930  
#accession B41367  
##molecule\_type mRNA  
##residues 317-482,'R',484-594 ##label MIC

REFERENCE A36463  
#authors Persson, H.; Peltto-Huikko, M.; Metsis, M.; Soeder, O.; Brene,  
S.; Skog, S.; Hoekfelt, T.; Ritzen, E.M.  
#journal Mol. Cell. Biol. (1990) 10:4701-4711  
#title Expression of the neurotransmitter-synthesizing enzyme  
glutamic acid decarboxylase in male germ cells.  
#cross-references MUID:90355986  
#accession A36463  
##molecule\_type mRNA  
##residues 527-594 ##label PER

REFERENCE A54778  
#cross-references GB:M55574; NID:g182929; PIDN:AAA72938.1; PID:g182930  
#authors Bu, D.F.; Tobin, A.J.  
#journal Genomics (1994) 21:222-228  
#title The exon-intron organization of the genes (GAD1 and GAD2)  
encoding two human glutamate decarboxylases (GAD-67 and  
GAD-65) suggests that they derive from a common ancestral  
GAD.

#cross-references MUID:94375018  
#contents annotation: intron-exon organization  
#comment This enzyme (GAD) catalyzes the formation of an inhibitory  
neurotransmitter, gamma-aminobutyric acid, from L-glutamic acid;  
it has several isoforms, each encoded by a separate gene. GAD has  
also been implicated as an autoantigen in autoimmune disease  
stiff-man syndrome and insulin-dependent diabetes mellitus.

GENETICS  
#gene GDB:GAD1; GAD  
#cross-references GDB:119244; OMIM:266100  
#map\_position 2q31-2q31  
CLASSIFICATION  
#superfamily human glutamate decarboxylase  
KEYWORDS  
alternative splicing; carbon-carbon lyase; carboxy-lyase;  
phosphoprotein; pyridoxal phosphate

FEATURE  
405  
#binding\_site pyridoxal phosphate (Lys) (covalent)  
#status predicted

SUMMARY  
#length 594 #molecular-weight 66924 #checksum 6189

Query Match 70.4%; Score 112; DB 1; Length 594;  
Best Local Similarity 70.0%; Pred. No. 3.06e-08;  
Matches 14; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Db 255 SNMYSIMAAKYKPEVKTR 274  
||||:|||||  
QY 1 SNMYSIMAAIRFKMPEVKKEK 20

RESULT 13  
ENTRY JG4065 #type complete  
TITLE glutamate decarboxylase (EC 4.1.1.15) 67k chain - pig  
ORGANISM #formal\_name Sus scrofa domestica #common\_name domestic pig  
DATE 30-Jun-1995 #sequence\_revision 14-Jul-1995 #text\_change

ACCESSIONS	22-Jun-1999
REFERENCE	JC4065
#authors	JC4064
#journal	Suzuki, R.; Asami, N.; Amann, E.; Wagatsuna, M.
#title	Gene (1995) 152:257-260
#accession	Sequences of 152 porcine glutamic acid decarboxylases (65-an
#cross-references	67-kDa GAD).
JC4065	67-kDa GAD).
#molecule-type	mRNA
#residues	1-594
#cross-references	DBJ:D31849; NID:q790966; PIDN:BAA06636.1;
#experimental	source brain
COMMENT	This enzyme catalyzes the conversion of glutamic acid into
CLASSIFICATION	gamma-amino butyric acid.
KEYWORDS	#superfamily human glutamate decarboxylase
FEATURE	carbon-carbon lyase; carboxy-lyase
402-405	#domain DOPA decarboxylase binding #status predicted
SUMMARY	#length 594 #molecular-weight 66894 #checksum 5491
Query Match	70.4%; Score 112; DB 2; Length 594;
Best Local Similarity	70.0%; Pred. No. 3,06e-08;
Matches	14; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
Db	255 SNMYSIMARKKYPPEVKTK 274
QY	1 SNMYAMMIAIRFKMPEVEK 20
RESULT	14
ENTRY	S51775
TITLE	#type complete
ORGANISM	glutamate decarboxylase (EC 4.1.1.15) - human
DATE	#formal_name Homo sapiens #common_name man
15-Jul-1995	#sequence_revision 21-Jul-1995 #text_change
22-Jun-1999	
ACCESSIONS	S51775
REFERENCE	S51775
#authors	Johnstone, A.
#submission	submitted to the EMBL Data Library, May 1993
#accession	S51775
##status	preliminary
##molecule-type	mRNA
##residues	1-594
##cross-references	EMBL:422150; NID:q298098; PIDN:CA80435.1;
PID:q298099	
CLASSIFICATION	#superfamily human glutamate decarboxylase
KEYWORDS	carbon-carbon lyase; carboxy-lyase
SUMMARY	#length 594 #molecular-weight 66973 #checksum 6437
Query Match	70.4%; Score 112; DB 2; Length 594;
Best Local Similarity	70.0%; Pred. No. 3,06e-08;
Matches	14; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
Db	255 SNMYSIMARKKYPPEVKTK 274
QY	1 SNMYAMMIAIRFKMPEVEK 20
RESULT	15
ENTRY	S71489
TITLE	#type complete
ALTERNATE_NAMES	sulfoalanine decarboxylase (EC 4.1.1.29) - rat
ORGANISM	cysteine sulfinate decarboxylase; cysteine sulfinic acid
DATE	decarboxylase
09-Dec-1997	#formal_name Rattus norvegicus #common_name Norway rat
22-Jun-1999	#sequence_revision 09-Dec-1997 #text_change
ACCESSIONS	S71489
REFERENCE	S71489
#authors	Reymond, I.; Sergeant, A.; Tappaz, M.
#journal	Biochim. Biophys. Acta (1996) 1307:152-156

```

#title Molecular cloning and sequence analysis of the cDNA encoding
#cross-references M01D:96283809 rat liver cysteine sulfinatase decarboxylase (CSD).
#accession S71489
##molecule_type mRNA
##residues 1-493 #label REV
##cross-references EMBL:X94152; NID:G1263163; P1DN:CAA63868.1;
PID:e218415; PID:g1263164
#experimental_source liver
#accession S78208
##molecule_type protein
##residues 9-22;106-124;467-484 #label REM
#REFERENCE S55689
#journal Katsakia, P.J.; Jenkins, A.A.; Goodspeed, D.C.; Steele, R.D.
#journal Biochim. Biophys. Acta (1995) 1262:79-82
#title Cloning and characterization of rat cysteine sulfinic acid
decarboxylase.
#cross-references M01D:95290499
#note the author's name has been corrected in reference S60723
#accession S55689
##molecule_type mRNA
##residues 1-177, 'V', 179-457, 'W', 459, 'PGPTSSMMMPPTPYMSRP' #label
KAI
##cross-references EMBL:M64755; NID:9847652; P1DN:AAC42063.1;
PID:g847653
#accession S55690
##status preliminary
##molecule_type protein
##residues 220-230 #label KA2
#REFERENCE S60723
#journal Katsaki, P.J.; Jenkins, A.A.; Goodspeed, D.C.; Steele, R.D.
#journal Biochim. Biophys. Acta (1995) 1263:179
#contents annotation; Erratum
#note this a correction of the author's name from reference S55689
CLASSIFICATION #superfamily human glutamate decarboxylase
KEYWORDS carbon-carbon lyase; carboxy-lyase; phosphoprotein; pyridoxa
phosphate
FEATURE
305 #binding-site pyridoxal phosphate (Lys) (covalent)
#status predicted
SUMMARY #length 493 #molecular-weight 55248 #checksum 7887
Query Match 57.2%; Score 91; DB 2; Length 493;
Best Local Similarity 50.0%; Pred. No. 3,18e-04;
Matches 10; Conservative 6; Mismatches 4; Indels 0; Gaps 0;
Db 155 SNNYAINLARFQRYPDCKOR 174
|||||:||||:|:|:
0Y 1 SNNYAMIMARKKPEYVEKK 20

```

Search completed: Tue Mar 7 21:16:14 2000  
Job time : 9 secs.



```

CC  Eur. J. Biochem. 212:597-603(1993).
CC  - FUNCTION: CATALYZES THE PRODUCTION OF GABA.
CC  - CATALYTIC ACTIVITY: L-GLUTAMATE - 4-AMINOBUTANOATE + CO(2).
CC  - COFACTOR: PYRIDOXAL PHOSPHATE.
CC  - SUBUNIT: HOMODIMER (BY SIMILARITY).
CC  - SIMILARITY: LOCAL TO DOPA DECARBOXYLASE, AND TO PLP-TYPE HISTIDINE
CC  DECARBOXYLASE.
CC  -----
CC  This SWISS-PROT entry is copyright. It is produced through a collaboration
CC  between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC  the European Bioinformatics Institute. There are no restrictions on its
CC  use by non-profit institutions as long as its content is in no way
CC  modified and this statement is not removed. Usage by and for commercial
CC  entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC  or send an email to license@isb-sib.ch).
CC  -----
CC  DR EMBL: M81882; AAA62367.1; -.
CC  DR EMBL: M74826; AAA58491.1; -.
CC  DR EMBL: X69936; CAA49554.1; ALT_INIT.
CC  DR EMBL: M70435; AAA52513.1; -.
CC  DR PIR: A41292; A41292.
CC  DR PIR: P00158; P00158.
CC  DR MIM: I38275; -.
CC  DR PROSITE: PS00392; DDC_GAD_HDC_YDC; 1.
CC  DR PFAM: PF00282; pyridoxal_dec; 1.
CC  DR Neurotransmitter biosynthesis; Lyase; Decarboxylase;
CC  KW Pyridoxal phosphate; Multigene family.
CC  FT BINDING 396 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
CC  SO SEQUENCE 585 AA; 65411 MW; 8AD62B62 CRC32;

Query Match 100.0%; Score 159; DB 1; Length 585;
Best Local Similarity 100.0%; Pred. No. 5,32e-21;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 246 SNMYAMTARFKPEVKEK 265
Qy 1 SNMYAMTARFKPEVKEK 20
|||||
RESULT 2
ID DCE2_PIG STANDARD: PRT; 585 AA.
AC P48321;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE GLUTAMATE DECARBOXYLASE, 65 KD ISOFORM (EC 4.1.1.15) (GAD-65)
DE (65 KD GLUTAMIC ACID DECARBOXYLASE).
GN GAD2 OR GAD65.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RX MEDLINE: 95137399.
RA SUZUKI R., ASAMI N., AMANN E., WACATSUNA M.;
RT "Sequences of two porcine glutamic acid decarboxylases (65- and
RT 67-kDa GAD).";
RL Gene 152:257-260(1995).
CC - FUNCTION: CATALYZES THE PRODUCTION OF GABA.
CC - CATALYTIC ACTIVITY: L-GLUTAMATE - 4-AMINOBUTANOATE + CO(2).
CC - COFACTOR: PYRIDOXAL PHOSPHATE.
CC - SUBUNIT: HOMODIMER (BY SIMILARITY).
CC - SIMILARITY: LOCAL TO DOPA DECARBOXYLASE, AND TO PLP-TYPE HISTIDINE
CC TYRDC).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).

```

```

CC  DR EMBL: D31848; BAA06635.1; -.
CC  DR PROSITE: PS00392; DDC_GAD_HDC_YDC; 1.
CC  DR PFAM: PF00282; pyridoxal_dec; 1.
CC  KW Neurotransmitter biosynthesis; Lyase; Decarboxylase;
CC  KW Pyridoxal phosphate; Multigene family.
CC  FT BINDING 396 PYRIDOXAL PHOSPHATE (POTENTIAL).
CC  SO SEQUENCE 585 AA; 65388 MW; F3E9BD88 CRC32;

Query Match 95.6%; Score 152; DB 1; Length 585;
Best Local Similarity 95.0%; Pred. No. 2,80e-19;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 246 SNMYAMTARFKPEVKEK 265
Qy 1 SNMYAMTARFKPEVKEK 20
|||||
RESULT 3
ID DCE2_MOUSE STANDARD: PRT; 585 AA.
AC P48320; Q35519;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-JUN-1998 (Rel. 36, Last annotation update)
DE GLUTAMATE DECARBOXYLASE, 65 KD ISOFORM (EC 4.1.1.15) (GAD-65)
DE (65 KD GLUTAMIC ACID DECARBOXYLASE).
GN GAD2 OR GAD65.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-C57BL/6; TISSUE-BRAIN;
RX MEDLINE: 94032481.
RA LEE D.S., TIAN J., PHAN T., KAUFMAN D.L.;
RT "Cloning and sequence analysis of a murine cDNA encoding glutamate
RT decarboxylase (GAD65).";
RL Biochim. Biophys. Acta 1216:157-160(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-C57BL/6; TISSUE-BRAIN;
RX MEDLINE: 97115675.
RA ASADA H., KANAMURA Y., MARYAMA K., KUME H., DING R.G., JI F.Y.,
RA KANBARA N., KUZOME H., SANBO M., YAGI T., OBATA K.;
RT "Mice lacking the 65 kDa isoform of glutamic acid decarboxylase
RT (GAD65) maintain normal levels of GAD67 and GABA in their brains but
RT are susceptible to seizures.";
RL Biochem. Biophys. Res. Commun. 229:891-895(1996).
RN [3]
RP SEQUENCE OF 175-379 FROM N.A.
RC TISSUE-BRAIN;
RX MEDLINE: 94062679.
RA FAULKNER-JONES B.E., CRAM D.S., KUN J., HARRISON L.C.;
RT "Localization and quantitation of expression of glutamate
RT decarboxylase genes in pancreatic beta-cells and other peripheral
RT tissues of mouse and rat.";
RL Endocrinology 133:2962-2972(1993).
CC - FUNCTION: CATALYZES THE PRODUCTION OF GABA.
CC - CATALYTIC ACTIVITY: L-GLUTAMATE - 4-AMINOBUTANOATE + CO(2).
CC - COFACTOR: PYRIDOXAL PHOSPHATE.
CC - SUBUNIT: HOMODIMER (BY SIMILARITY).
CC - SIMILARITY: LOCAL TO DOPA DECARBOXYLASE, AND TO PLP-TYPE HISTIDINE
CC DECARBOXYLASE.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC  EMBL: L16980; AAA93049.1; -.

```

```

DR EMBL: D42051: BAA22893.1: -.
DR EMBL: S67454: CAB32806.1: -.
DR MGI: 95634; GAD2.
DR PROSITE: PS00392; DDC_GAD_HDC_YDC: 1.
DR PFAM: PF00282; Pyridoxal dec: 1.
KW Neurotransmitter biosynthesis; Lyase: Decarboxylase;
KW Pyridoxal phosphate; Multigene family.
FT BINDING 396 396 PYRIDOXAL PHOSPHATE (POTENTIAL).
FT CONFLICT 259 259 F -> S (IN REF. 2).
FT CONFLICT 319 319 I -> S (IN REF. 3).
FT CONFLICT 325 325 K -> E (IN REF. 2).
FT CONFLICT 499 499 P -> S (IN REF. 2).
FT SEQUENCE 585 AA: 65224 MW: 985088 CRC32:
Query Match 93.1%; Score 148; DB 1; Length 585;
Best Local Similarity 90.0%; Pred. No. 2,65e-18;
Matches 18; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 246 SNMYAMLIARKMPPEVKEK 265
QY 1 SNMYAMLIARKMPPEVKEK 20
RESULT 4
ID DCE2_RAT STANDARD: PRT: 585 AA.
AC Q05683;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE GLUTAMATE DECARBOXYLASE, 65 KD ISOFORM (EC 4.1.1.15) (GAD-65)
DE (65 KD GLUTAMIC ACID DECARBOXYLASE).
GN GAD2 OR GAD65.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-HIPPOCAMPUS;
RA ERLANDER M.G., TILAKARATNE N.J., FELDBLUM S., PATEL N.,
RA TOBIN A.J.;
RT "Two genes encode distinct glutamate decarboxylases.";
RL Neuron 7:91-100(1991).
CC -1- FUNCTION: CATALYZES THE PRODUCTION OF GABA.
CC -1- CATALYTIC ACTIVITY: L-GLUTAMATE = 4-AMINOBUTANOATE + CO(2).
CC -1- COFACTOR: PYRIDOXAL PHOSPHATE.
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SIMILARITY: LOCAL TO DOPA DECARBOXYLASE, AND TO PLP-TYPE HISTIDINE
CC DECARBOXYLASE.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: M72422: AAA63488.1: -.
DR PROSITE: PS00392; DDC_GAD_HDC_YDC: 1.
DR PFAM: PF00282; pyridoxal dec: 1.
KW Neurotransmitter biosynthesis; Lyase: Decarboxylase;
KW Pyridoxal phosphate; Multigene family.
FT BINDING 396 396 PYRIDOXAL PHOSPHATE (POTENTIAL).
FT SEQUENCE 585 AA: 65402 MW: 8350601A CRC32:
Query Match 93.1%; Score 148; DB 1; Length 585;
Best Local Similarity 90.0%; Pred. No. 2,65e-18;
Matches 18; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 246 SNMYAMLIARKMPPEVKEK 265
QY 1 SNMYAMLIARKMPPEVKEK 20

```

```

RESULT 5
ID DCE1_FELCA STANDARD: PRT: 594 AA.
AC P14748;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE GLUTAMATE DECARBOXYLASE, 67 KD ISOFORM (EC 4.1.1.15) (GAD-67)
DE (67 KD GLUTAMIC ACID DECARBOXYLASE).
GN GAD1 OR GAD67.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;
OC Eutheria; Carnivora; Fissipedia; Felidae; Felis.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-OCCIPITAL CORTEX;
RX MEDLINE: 87310623;
RA KOBAYASHI Y., KAUFMAN D.L., TOBIN A.J.;
RT "Glutamic acid decarboxylase cDNA: nucleotide sequence encoding an
RT enzymatically active fusion protein.";
RL J. Neurosci. 7:2768-2772(1987).
CC -1- FUNCTION: CATALYZES THE PRODUCTION OF GABA.
CC -1- CATALYTIC ACTIVITY: L-GLUTAMATE = 4-AMINOBUTANOATE + CO(2).
CC -1- COFACTOR: PYRIDOXAL PHOSPHATE.
CC -1- SUBUNIT: HOMODIMER.
CC -1- SIMILARITY: BELONGS TO GROUP II DECARBOXYLASES (DDC, GAD, HDC AND
CC TYRDC).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: M18629: AAA51430.1: -.
DR PIR: A45671; A45671.
DR PIR: A46758; A46758.
DR PROSITE: PS00392; DDC_GAD_HDC_YDC: 1.
DR PFAM: PF00282; pyridoxal dec: 1.
KW Neurotransmitter biosynthesis; Lyase: Decarboxylase;
KW Pyridoxal phosphate; Multigene family.
FT BINDING 405 405 PYRIDOXAL PHOSPHATE (POTENTIAL).
FT SEQUENCE 594 AA: 66824 MW: 3EC20778 CRC32:
Query Match 73.0%; Score 116; DB 1; Length 594;
Best Local Similarity 70.0%; Pred. No. 9,26e-11;
Matches 14; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Db 255 SNMYSIMARKMPPEVYTK 274
QY 1 SNMYSIMARKMPPEVYTK 20
RESULT 6
ID DCE1_MOUSE STANDARD: PRT: 593 AA.
AC P48318;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE GLUTAMATE DECARBOXYLASE, 67 KD ISOFORM (EC 4.1.1.15) (GAD-67)
DE (67 KD GLUTAMIC ACID DECARBOXYLASE).
GN GAD1 OR GAD67.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RA KARAROVA Z., SZABO G., MUGNAINI E., GREENSPAN R.;
RT "Molecular identification of the 62 kd form of glutamic acid

```

RT decarboxylase from the mouse."  
RL Eur. J. Neurosci. 2:190-202(1990).  
RN [2]  
RP SEQUENCE OF 198-403 FROM N.A.  
RC TISSUE-BRAIN;  
RX MEDLINE: 94062679.  
RA FAULKNER-JONES B.E., GRAM D.S., KUN J., HARRISON L.C.;  
RT "Localisation and quantitation of expression of two glutamate  
decarboxylase genes in pancreatic beta-cells and other peripheral  
tissues of mouse and rat."  
RL Endocrinology 133:2962-2972(1993).  
CC -1- FUNCTION: CATALYZES THE PRODUCTION OF GABA.  
CC -1- CATALYTIC ACTIVITY: L-GLUTAMATE = 4-AMINOBUTANOATE + CO(2).  
CC -1- CORYCTOR: PYRIDOXAL PHOSPHATE.  
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).  
CC -1- SIMILARITY: BELONGS TO GROUP II DECARBOXYLASES (DDC, GAD, HDC AND TYROC).  
-----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
-----  
CC EMBL: Z4976; CAA90277.1; -  
DR EMBL: S67453; CAB32805.1; -  
DR MGI: 95632; GAD1.  
DR PROSITE: PS00392; DDC\_GAD\_HDC\_YDC; 1.  
DR PFAM: PF00282; pyridoxal\_dec; 1.  
KW Neurotransmitter biosynthesis; Lyase; Decarboxylase;  
KW Pyridoxal phosphate; Multigene family.  
FT BINDING 404  
FT CONFLICT 234 E -> K (IN REF. 2).  
FT CONFLICT 258 S -> T (IN REF. 1).  
FT CONFLICT 360 D -> S (IN REF. 1).  
SQ SEQUENCE 593 AA; 66584 MW; 63BC579A CRC32;  
  
Query Match 70.4%; Score 112; DB 1; Length 593;  
Best Local Similarity 70.0%; Pred. No. 7, 41e-10;  
Matches 14; Conservative 3; Mismatches 3; Indels 0; Gaps 0;  
  
Db 254 SNNYSIMARKYFFPEVTK 273  
QY 1 SNNYAMMIARFKMFPEVKEK 20  
||||:|||||  
  
RESULT 7  
ID DCEL-RAT STANDARD; PRT; 593 AA.  
AC P18088;  
DT 01-NOV-1990 (Rel. 16, Created)  
DT 01-NOV-1990 (Rel. 16, Last sequence update)  
DT 01-FEB-1996 (Rel. 33, Last annotation update)  
DE GLUTAMATE DECARBOXYLASE, 67 KD ISOFORM (EC 4.1.1.15) (GAD-67)  
DE (67 KD GLUTAMIC ACID DECARBOXYLASE).  
GN GAD1 OR GAD67.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE: 91014554.  
RA WYBORSKI R.J., BOND R.W., GOTTLEB D.I.;  
RT "Characterization of a cDNA coding for rat glutamic acid  
decarboxylase".  
RL Brain Res. Mol. Brain Res. 8:193-198(1990).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE: 90132703.  
RA JULIEN J.F., SAMAMA P., MALLET J.;  
RT "Rat brain glutamic acid decarboxylase sequence deduced from a cloned  
cDNA.";

RL J. Neurochem. 54:703-705(1990).  
RN [3]  
RP SEQUENCE FROM N.A.  
RX MEDLINE: 92020930.  
RA MICHELSEN B.K., PETERSEN J.S., BOEL E., MOLDROP A., DYBERG T.,  
RA MADSEN O.D.;  
RT "Cloning, characterization, and autoimmune recognition of rat islet  
glutamic acid decarboxylase in insulin-dependent diabetes mellitus".  
RL Proc. Natl. Acad. Sci. U.S.A. 88:8754-8758(1991).  
CC -1- FUNCTION: CATALYZES THE PRODUCTION OF GABA.  
CC -1- CATALYTIC ACTIVITY: L-GLUTAMATE = 4-AMINOBUTANOATE + CO(2).  
CC -1- CORYCTOR: PYRIDOXAL PHOSPHATE.  
CC -1- SUBUNIT: HOMODIMER.  
CC -1- SIMILARITY: BELONGS TO GROUP II DECARBOXYLASES (DDC, GAD, HDC AND TYROC).  
-----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
-----  
CC EMBL: M34445; AAC42037.1; -  
DR EMBL: X57572; CAA40800.1; -  
DR EMBL: X57573; CAA40801.1; -  
DR EMBL: M76177; AAA41184.1; -  
DR PIR: A41367; A41367.  
DR PIR: A43756; A43756.  
DR PROSITE: PS00392; DDC\_GAD\_HDC\_YDC; 1.  
DR PFAM: PF00282; pyridoxal\_dec; 1.  
KW Neurotransmitter biosynthesis; Lyase; Decarboxylase;  
KW Pyridoxal phosphate; Multigene family.  
FT BINDING 404  
FT CONFLICT 103 404  
FT CONFLICT 284 103  
FT CONFLICT 284 284  
FT CONFLICT 287 288  
FT CONFLICT 344 345  
FT CONFLICT 347 347  
FT CONFLICT 352 353  
FT CONFLICT 380 380  
SQ SEQUENCE 593 AA; 66640 MW; 5A0B67C0 CRC32;  
  
Query Match 70.4%; Score 112; DB 1; Length 593;  
Best Local Similarity 70.0%; Pred. No. 7, 41e-10;  
Matches 14; Conservative 3; Mismatches 3; Indels 0; Gaps 0;  
  
Db 254 SNNYSIMARKYFFPEVTK 273  
QY 1 SNNYAMMIARFKMFPEVKEK 20  
||||:|||||  
  
RESULT 8  
ID DCEL-HUMAN STANDARD; PRT; 594 AA.  
AC Q99259;  
DT 01-FEB-1996 (Rel. 33, Created)  
DT 01-FEB-1996 (Rel. 33, Last sequence update)  
DT 01-OCT-1996 (Rel. 34, Last annotation update)  
DE GLUTAMATE DECARBOXYLASE, 67 KD ISOFORM (EC 4.1.1.15) (GAD-67)  
DE (67 KD GLUTAMIC ACID DECARBOXYLASE).  
GN GAD1 OR GAD.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
OC Eutheria; Primates; Catarrhini; Homiidae; Homo.  
RN [1]  
RP SEQUENCE FROM N.A.  
RX TISSUE-BRAIN;  
RC MEDLINE: 92196068.  
RA BU D.-F., ERLANDER M.G., HITZ B.C., TILAKARATNE N.J., KAUFMAN D.L.,  
RA WAGNER-MCPHERSON C.B., EVANS G.A., TOBIN A.J.;  
RT "Two human glutamate decarboxylases, 65-kDa GAD and 67-kDa GAD, are  
each encoded by a single gene.";



Proc. Natl. Acad. Sci. U.S.A. 89:2115-2119(1992).  
[2] SEQUENCE FROM N.A.  
MEDLINE: 94375018.  
RA BU D.-F., TOBIN A.J.;  
RT "The exon-intron organization of the genes (GAD1 and GAD2) encoding two human glutamate decarboxylases (GAD67 and GAD65) suggests that they derive from a common ancestral GAD.";  
RL Genomics 21:222-228(1994).  
[3] SEQUENCE FROM N.A.  
RC TISSUE-BRAIN;  
RX MEDLINE: 93060286.  
RA KELLY C.D., EDWARDS Y., JOHNSTONE A.P., HARFEST E., NOGRADI A., NUSSER S.S., POVEY S., CARTER N.D.;  
RT "Nucleotide sequence and chromosomal assignment of a cDNA encoding the large isoform of human glutamate decarboxylase.";  
RL Ann. Hum. Genet. 56:255-265(1992).  
[4] SEQUENCE FROM N.A.  
RX MEDLINE: 93282844.  
RA YAMASHITA K., GRAM D.S., HARRISON L.C.;  
RT "Molecular cloning of full-length glutamic acid decarboxylase 67 from human pancreas and islets.";  
RL Biochem. Biophys. Res. Commun. 192:1347-1352(1993).  
[5] SEQUENCE FROM N.A.  
RC TISSUE-PANCREATIC ISLETS;  
RX MEDLINE: 93282845.  
RA KAMASAKI E., MORICHI R., WATANABE M., SATOH K., BRUNICARDI F.C., WATT P.C., YAMAGUCHI T., MULLEN Y., AKAZAWA S., MIYAMOTO T.;  
RT "Cloning and expression of large isoform of glutamic acid decarboxylase from human pancreatic islet.";  
RL Biochem. Biophys. Res. Commun. 192:1353-1359(1993).  
[6] SEQUENCE FROM N.A.  
RA GIORDA R., PEARMAN M., VERGANI D., TRUCCO M.;  
RT Submitted (MAR-1992) to the EMBL/GenBank/DBJ databases.  
[7] SEQUENCE OF 218-397 FROM N.A.  
RC TISSUE-BRAIN;  
RX MEDLINE: 91248209.  
RA CRAM D.S., BARRETT L.D., JOSEPH J.L., HARRISON L.C.;  
RT "Cloning and partial nucleotide sequence of human glutamic acid decarboxylase cDNA from brain and pancreatic islets.";  
RL Biochem. Biophys. Res. Commun. 176:1239-1244(1991).  
[8] SEQUENCE OF 527-594 FROM N.A.  
RC TISSUE-TESTIS;  
RX MEDLINE: 90353986.  
RA SKOG S., HOEKFELT T., RITZEN E.M.;  
RT "Expression of the neurotransmitter-synthesizing enzyme glutamic acid decarboxylase in male germ cells.";  
RL Mol. Cell. Biol. 10:4701-4711(1990).  
[9] FUNCTION: CATALYZES THE PRODUCTION OF GABA.  
[10] CATALYTIC ACTIVITY: L-GLUTAMATE + CO(2).  
[11] COFACTOR: PYRIDOXAL PHOSPHATE.  
[12] SUBUNIT: HOMODIMER.  
[13] SIMILARITY: BELONGS TO GROUP II DECARBOXYLASES (DDC, GAD, HDC AND TYROC).  
-----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
-----  
CC EMBL: M81883: AAA62368.1: -  
DR EMBL: L16888: AAB59427.1: -  
EMBL: 222750: CAA80435.1: -

DR EMBL: S61897: AAB26937.1: -  
DR EMBL: S61896: AAB26938.1: -  
DR EMBL: M86522: AAA35900.1: -  
DR EMBL: M70434: AAA52512.1: -  
DR EMBL: M55574: AAA72938.1: -  
DR EMBL: A28074: CAA01913.1: -  
DR PIR: P00157: P00157.  
DR MIM: 266100: -  
DR PROSITE: PS00392: DDC\_GAD\_HDC\_YDC: 1.  
DR PFAM: PF00282: pyridoxal\_dec: 1.  
KM Neurotransmitter biosynthesis: Lysase; Decarboxylase;  
KW pyridoxal phosphate; Multigene family.  
FT BINDING 405 405  
FT CONFLICT 9 9  
FT CONFLICT 16 17  
FT CONFLICT 17 17  
FT CONFLICT 17 17  
FT CONFLICT 18 18  
FT CONFLICT 31 31  
FT CONFLICT 68 68  
FT CONFLICT 116 116  
FT CONFLICT 136 136  
FT CONFLICT 140 140  
FT CONFLICT 142 142  
FT CONFLICT 155 155  
FT CONFLICT 206 206  
FT CONFLICT 302 302  
FT CONFLICT 436 436  
FT CONFLICT 512 512  
FT CONFLICT 477 477  
FT CONFLICT 492 492  
FT CONFLICT 565 565  
SQ SEQUENCE 594 AA: 66896 MM: 9473352 CRC32:  
Query Match 70.4%: Score 112: DB 1: Length 594:  
Best Local Similarity 70.0%: Pred. No. 7,41e-10:  
Matches 14: Conservative 3: Mismatches 3: Indels 0: Gaps 0:  
DB 255 SNMYSIMARKYKPEVYK 274  
QY 1 SNMYSIMARKYKPEVYK 20  
|||||:|||||  
ID DEEL\_PIG STANDARD: PRT: 594 AA.  
AC P48319;  
DT 01-FEB-1996 (Rel. 33, Created)  
DT 01-FEB-1996 (Rel. 33, Last sequence update)  
DT 01-FEB-1996 (Rel. 33, Last annotation update)  
DE GLUTAMATE DECARBOXYLASE, 67 KD ISOFORM (EC 4.1.1.15) (GAD-67)  
DE (67 KD GLUTAMIC ACID DECARBOXYLASE).  
GN GAD1 OR GAD67.  
OS Sus scrofa (Pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
OC Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE-BRAIN;  
RX MEDLINE: 95137399.  
RA SUZUKI R., ASAMI N., AMANN E., WAGATSUMA M.;  
RT "Sequences of two porcine glutamic acid decarboxylases (65- and 67-kDa GAD).";  
RL Gene 152:257-260(1995).  
[9] FUNCTION: CATALYZES THE PRODUCTION OF GABA.  
[10] CATALYTIC ACTIVITY: L-GLUTAMATE + CO(2).  
[11] COFACTOR: PYRIDOXAL PHOSPHATE.  
[12] SUBUNIT: HOMODIMER (BY SIMILARITY).  
[13] SIMILARITY: BELONGS TO GROUP II DECARBOXYLASES (DDC, GAD, HDC AND TYROC).  
-----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way

CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL: D31849; BAA06636.1; -  
 DR PROSITE: PS00392; DDC\_GAD\_HDC\_YDC. 1.  
 DR PFAM: PF00282; Pyridoxal-dec. 1.  
 DR Neurotransmitter biosynthesis; Lyase; Decarboxylase;  
 DR Pyridoxal phosphate; Multiligene family.  
 FT BINDING 405 405 PYRIDOXAL PHOSPHATE (POTENTIAL).  
 SO SEQUENCE 594 AA; 66894 MW; 69D6C79C CRC32;  
 Query Match 70.4%; Score 112; DB 1; Length 594;  
 Best Local Similarity 70.0%; Pred. No. 7.41e-10;  
 Matches 14; Conservative 3; Mismatches 3; Indels 0; Gaps 0;  
 Db 255 SNMYSIMARARYKPEVKT 274  
 1 SNMYSIMARARYKPEVKEK 20  
 Oy 1 SNMYSIMARARYKPEVKEK 20  
 RESULT 10  
 ID DCE\_DROME STANDARD; PRT; 510 AA.  
 AC P20228;  
 DT 01-FEB-1991 (Rel. 17, Created)  
 DT 01-FEB-1991 (Rel. 17, Last sequence update)  
 DT 01-NOV-1995 (Rel. 32, Last annotation update)  
 DE GLUTAMATE DECARBOXYLASE (EC 4.1.1.15) (GAD).  
 GN GAD OR GLB.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Ephygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephygoidae; Drosophilidae; Drosophila.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE: 90155291.  
 RA JACKSON F.R., NEWBY L.M., KULKARNI S.J.;  
 RT "Drosophila GABAergic systems: sequence and expression of glutamic  
 RT acid decarboxylase";  
 RL J. Neurochem. 54:1068-1078(1990).  
 CC -1- FUNCTION: CATALYZES THE PRODUCTION OF GABA.  
 CC -1- CATALYTIC ACTIVITY: L-GLUTAMATE = 4-AMINOBUTANOATE + CO(2).  
 CC -1- COFACTOR: PYRIDOXAL PHOSPHATE.  
 CC -1- SUBUNIT: HOMODIMER.  
 CC -1- SIMILARITY: BELONGS TO GROUP II DECARBOXYLASES (DDC, GAD, HDC AND  
 CC TYRDC).  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL: X76198; CA53791.1; -  
 DR PIR: A30999; A30999.  
 DR PIR: JH0192; JH0192.  
 DR FLYBASE: FBgn004516; Gad1.  
 DR PROSITE: PS00392; DDC\_GAD\_HDC\_YDC. 1.  
 DR PFAM: PF00282; Pyridoxal-dec. 1.  
 DR Neurotransmitter biosynthesis; Lyase; Decarboxylase;  
 DR Pyridoxal phosphate.  
 FT BINDING 322 322 PYRIDOXAL PHOSPHATE (POTENTIAL).  
 SO SEQUENCE 510 AA; 57758 MW; 97C7ABF1 CRC32;  
 Query Match 55.3%; Score 88; DB 1; Length 510;  
 Best Local Similarity 63.2%; Pred. No. 1.07e-04;  
 Matches 12; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
 Db 170 SNLYAFIARHKMPYKE 188  
 1 SNMYSIMARARYKPEVKE 19  
 Oy 1 SNMYSIMARARYKPEVKE 19

RESULT 11  
 ID MAK\_MOUSE STANDARD; PRT; 622 AA.  
 AC 004859;  
 DT 01-FEB-1994 (Rel. 28, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 01-NOV-1997 (Rel. 35, Last annotation update)  
 DE SERINE/THREONINE-PROTEIN KINASE MAK (EC 2.7.1.-) (MALE GERM CELL-  
 DE ASSOCIATED KINASE) (PROTEIN KINASE RCK).  
 GN MAK OR RCK.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE: 93366030.  
 RA BLADT F., BIRCHMEIER C.;  
 RT "Characterization and expression analysis of the murine rck gene: a  
 RT protein kinase with a potential function in sensory cells";  
 RL Differentiation 53:115-122(1993).  
 CC -1- FUNCTION: COULD HAVE AN IMPORTANT FUNCTION IN SIGNALING PATHWAYS USED  
 CC IN SPERMATOGENESIS. MAY PARTICIPATE IN SIGNALING PATHWAYS USED  
 CC IN VISUAL AND OLFACTORY SENSORY TRANSDUCTION.  
 CC -1- TISSUE SPECIFICITY: IN PRE- AND POSTMEIOTIC MALE GERM CELLS IN  
 CC TESTIS. IN PHOTORECEPTOR CELLS OF THE RETINA AND IN THE OLFACTORY  
 CC RECEPTORS, AND IN CERTAIN EPITHELIA OF THE RESPIRATORY TRACT  
 CC AND CHOROID PLEXUS (BRAIN).  
 CC -1- DEVELOPMENTAL STAGE: ON DAY 14 OR 17 OF EMBRYONIC DEVELOPMENT.  
 CC -1- SIMILARITY: BELONGS TO THE CDC2/CDC28 SUBFAMILY OF SER/THR  
 CC PROTEIN KINASES. BELONGS TO THE CDC2/CDKX SUBFAMILY.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL: X66983; CAA47392.1; -  
 DR PIR: S24241; S24241.  
 DR HSSP: P24941; IAO1.  
 DR MGD: MGT:96913; MAK.  
 DR PROSITE: PS00107; PROTEIN\_KINASE\_ATP. 1.  
 DR PROSITE: PS00108; PROTEIN\_KINASE\_ST. 1.  
 DR PROSITE: PS50011; PROTEIN\_KINASE\_DOM. 1.  
 DR PFAM: PF00069; Pkinase. 1.  
 DR Transferase; Serine/threonine-protein kinase; ATP-binding.  
 FT DOMAIN 4 284 PROTEIN KINASE.  
 FT NP\_BIND 10 18 ATP (BY SIMILARITY).  
 FT BINDING 33 33 ATP (BY SIMILARITY).  
 FT ACT\_SITE 125 125 BY SIMILARITY.  
 FT DOMAIN 309 368 GLU/PRO-RICH.  
 SO SEQUENCE 622 AA; 70050 MW; A3D11D70 CRC32;  
 Query Match 45.3%; Score 72; DB 1; Length 622;  
 Best Local Similarity 53.3%; Pred. No. 1.36e-01;  
 Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
 Db 85 NLYQAMKRNKLPPE 99  
 2 NMYAMIMARARYKPE 16  
 Oy 2 NMYAMIMARARYKPE 16  
 RESULT 12  
 ID MAK\_RAT STANDARD; PRT; 622 AA.  
 AC P20793;  
 DT 01-FEB-1991 (Rel. 17, Created)  
 DT 01-FEB-1991 (Rel. 17, Last sequence update)  
 DT 01-NOV-1997 (Rel. 35, Last annotation update)  
 DE SERINE/THREONINE-PROTEIN KINASE MAK (EC 2.7.1.-) (MALE GERM CELL-  
 DE ASSOCIATED KINASE).  
 GN MAK OR RCK.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

```

RT "Complete genome sequence of the methanogenic archaeon, Methanococcus
RT jannaschii."
RL Science 273:1058-1073(1996).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U67515; AAB96861.1; -.
DR TIGR; MJO686; -.
KW Hypothetical protein.
SQ SEQUENCE 580 AA; 68392 MW; 5C3F000E CRC32;

Query Match 41.5%; Score 65; DB 1; Length 580;
Best Local Similarity 41.2%; Pred. No. 1.59e+00;
Matches 7; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

Dd 239 YDLVARYKFKIKLREK 255
|:::|::|:|:|:|
Oy 4 YAMMIAKRPKEPEVKEK 20

RESULT 14 STANDARD; PRT; 587 AA.
ID YID6_YEAST
AC P40535;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE HYPOTHEETICAL 65.3 KD PROTEIN IN NOT3-CYAL INTERGENIC REGION.
GN YII038W.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Hemiascomycetes; Saccharomycetales;
OC Saccharomycetaceae; Saccharomycetes.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-S288C / AB972;
RC BARRELL B.G., BADCOCK K., BANKIER A.T., BOWMAN S., BROWN D.,
RA CHURCHER C.M., CONNOR R., COPELY T., DEAR S., DEVLIN K., FRASER A.,
RA GENTLES S., HAMLYN N., HORSNELL T.S., HUNT S., JAGELS K., JONES M.,
RA LOUIS E., LYE G., MOULE S., MOULE T., ODELL C., PEARSON D.,
RA RAJANAREAN M.A., RILES L., ROWLEY N., SKELTON J., SMITH V.,
RA WALSH S.V., WHITEHEAD S.;
RL Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: TO YEAST YER045C.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; Z46861; CA86915.1; -.
DR PFAM; PF00170; bZIP; 1.
KW Hypothetical protein; ATP-binding.
FT NP_BIND 382 389 ATP (POTENTIAL).
SQ SEQUENCE 587 AA; 65264 MW; 3D0AA705 CRC32;

Query Match 40.9%; Score 65; DB 1; Length 587;
Best Local Similarity 35.7%; Pred. No. 2.37e+00;
Matches 5; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

Dd 474 YEKLSIKKKFKFSKI 487
|:::|::|:|:|:|
Oy 4 YAMMIAKRPKEPEV 17

```

```

ID KIME METH STANDARD: PR1: 303 AA.
AC Q50559: Q26152:
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE MEVALONATE KINASE (EC 2.7.1.36) (MK).
GN MTH46.
OS Methanobacterium thermoautotrophicum.
OC Archaea: Euryarchaeota: Methanobacteriales: Methanobacteriaceae:
OC Methanobacterium.
[1]
RN SEQUENCE FROM N.A.
RC STRAIN-DELTA H:
RA SHARMA S., REEVE J.N.;
RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
[2]
RN SEQUENCE FROM N.A.
RP STRAIN-DELTA H:
RX MEDLINE: 98037514.
RA SMITH D.R., DOUCETTE-STAMM L.A., DELOUGHERY C., LEE H.-M., DUBOIS J.,
RA ALBRECHT T., BASHIRZADEH R., BLAKELY D., COOK R., GILBERT K.,
RA HARRISON D., HOANG L., KEAGLE P., LUMM W., POTHIER B., QIU D.,
RA SPADAFORA R., VICARE R., WANG Y., WIERZBOWSKI J., GIBSON R.,
RA JIWANI N., CARUSO A., BUSH D., SAFER H., PATWELL D., PRABHAKAR S.,
RA MCDONUGALL S., SHIMER G., GOYAL A., PIETROVSKI S., CHURCH G.M.,
RA DANIELS C.J., MAO J.-I., RICE P., NOLLING J., REEVE J.N.;
RT "Complete genome sequence of Methanobacterium thermoautotrophicum
RT delah: functional analysis and comparative genomics.";
RL J. Bacteriol. 179:7135-7155(1997).
CC -I- CATALYTIC ACTIVITY: ATP + (R)-MEVALONATE = ADP +
CC (R)-5-PHOSPHOMEVALONATE.
CC -I- SIMILARITY: TO OTHER SPECIES MEVALONATE KINASE.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U47134; AAA87051.1; -
DR EMBL: AE000796; AAB84553.1; -
DR PROSITE: PS00627; GHMP_KINASES_ATP; 1.
KW Transferase; Kinase; ATP-binding.
FT NP_BIND 90 100 ATP (POTENTIAL).
FT CONFLICT 108 108 A -> P (IN REF. 2).
SQ SEQUENCE 303 AA; 32224 MW; DAA8B6D9 CRC32;

```

Query Match 40.3%; Score 64; DB 1; Length 303;  
 Best local Similarity 30.0%; Pred. No. 3.50e+00;  
 Matches 6; Conservative 7; Mismatches 7; Indels 0; Gaps 0;  
 Db 181 AAMVAGVAERFRPPDIMG 200  
 QY 1 SMTYAMMTARFKMPPEVK 20

Search completed: Tue Mar 7 21:15:47 2000  
 Job time : 6 secs.

Release 3.1A John F. Collins, Biocomputing Research Unit.  
Copyright (c) 1993-1998 University of Edinburgh, U.K.  
Distribution Rights by Oxford Molecular Ltd

(TM)

\*\*\*\*\*

Release 3.1A John F. Collins, Biocomputing Research Unit.  
Copyright (c) 1993-1998 University of Edinburgh, U.K.  
Distribution Rights by Oxford Molecular Ltd

Msrch\_bp protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Mar 7 21:15:14 2000: MasPar time 6.74 Seconds

Tabular output not generated. 205,845 Million cell updates/sec

Title: &gt;US-08-981-824-2

Description: (1-20) from US08981824.pep

Perfect Score: 159

Sequence: 1 SNMYAMMIARFKMFPEVK 20

Scoring table:

PAM 150  
Gap 15

Searched: 225878-segs, 69334122 residues

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database:

sptrembl12

1:sp:archaea 2:sp:bacteria 3:sp:fungi 4:sp:human

5:sp:invertebrate 6:sp:mammal 7:sp:mhc 8:sp:organelle

9:sp:phage 10:sp:plant 11:sp:rodent 12:sp:unclassified

13:sp:vertebrate 14:sp:virus

Statistics: Mean 29.459; Variance 46.484; scale 0.634

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	152	95.6	182	13	09W661	GLUTAMATE DECARBOXYLASE 1.86e-17
2	152	95.6	182	13	09W659	GLUTAMATE DECARBOXYLASE 1.86e-17
3	143	88.9	182	13	09W654	GLUTAMATE DECARBOXYLASE 1.92e-15
4	143	88.9	232	13	09J275	GLUTAMATE DECARBOXYLASE 1.92e-15
5	126	75.2	182	13	09W656	GLUTAMATE DECARBOXYLASE 2.46e-14
6	126	75.2	182	13	09W657	GLUTAMATE DECARBOXYLASE 1.01e-11
7	118	74.2	182	13	09W655	GLUTAMATE DECARBOXYLASE 5.15e-10
8	118	74.2	232	13	09J276	GLUTAMATE DECARBOXYLASE 5.15e-10
9	112	70.4	182	13	09W660	GLUTAMATE DECARBOXYLASE 9.33e-09
10	112	70.4	182	13	09W663	GLUTAMATE DECARBOXYLASE 9.33e-09
11	112	70.4	563	13	09I158	GLUTAMATE DECARBOXYLASE 9.33e-09
12	112	70.4	590	13	09Y158	GLUTAMATE DECARBOXYLASE 9.33e-09
13	112	70.4	593	13	09B685	67KD GLUTAMATE DECARBOXYLASE 9.33e-09
14	107	67.3	182	13	09W658	GLUTAMATE DECARBOXYLASE 1.00e-07
15	91	57.2	478	11	064577	CYSTEINE SULFINIC ACID 1.54e-04
16	91	57.2	493	11	064611	CYSTEINE SULFINIC ACID 1.54e-04
17	88	55.3	370	5	044102	GLUTAMATE DECARBOXYLASE 5.80e-04
18	88	55.3	370	5	044103	GLUTAMATE DECARBOXYLASE 5.80e-04
19	87	54.7	267	4	09Y602	CYSTEINE SULFINIC ACID 8.97e-04
20	87	54.7	493	4	09Y600	CYSTEINE SULFINIC ACID 8.97e-04

RESULT ID	1	PRELIMINARY	PRT	182 AA
AC	09W661			
DT	01-NOV-1999	(TREMBLrel. 12, Created)		
DT	01-NOV-1999	(TREMBLrel. 12, Last sequence update)		
DT	01-NOV-1999	(TREMBLrel. 12, Last annotation update)		
DE	GLUTAMATE DECARBOXYLASE ISOFORM 65 (EC 4.1.1.15) (FRAGMENT).			
GN	GAD65.			
OS	Pseudomyrmex scripta (Slider turtle).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Testudines;			
CC	Cryptodira; Testudinoidae; Emydidae; Testudines;			
RM	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE-BRAIN;			
RX	MEDLINE; 99261650.			
RA	BOSMA P.T., BLAZQUEZ M., COLLINS M.A., BISHOP J.D., DROUIN G.,			
RA	PRIDE I.G., DOCHERRY K., TRUDEAU V.L.;			
RT	"Multiplication of glutamic acid decarboxylases (GAD) in vertebrates:			
RT	molecular phylogeny and evidence for a new GAD paralog."			
RL	Mol. Biol. Evol. 16:397-404(1999).			
DR	EMBL; AF043272; AAD22718.1;			
KW	Lyase.			
FT	NON TER			
FT	NON TER			
SO	SEQUENCE	182 AA; 19942 MW; 1699125D CRC32;		

## ALIGNMENTS

RESULT ID	1	PRELIMINARY	PRT	182 AA
AC	09W661			
DT	01-NOV-1999	(TREMBLrel. 12, Created)		
DT	01-NOV-1999	(TREMBLrel. 12, Last sequence update)		
DT	01-NOV-1999	(TREMBLrel. 12, Last annotation update)		
DE	GLUTAMATE DECARBOXYLASE ISOFORM 65 (EC 4.1.1.15) (FRAGMENT).			
GN	GAD65.			
OS	Pseudomyrmex scripta (Slider turtle).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Testudines;			
CC	Cryptodira; Testudinoidae; Emydidae; Testudines;			
RM	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE-BRAIN;			
RX	MEDLINE; 99261650.			
RA	BOSMA P.T., BLAZQUEZ M., COLLINS M.A., BISHOP J.D., DROUIN G.,			
RA	PRIDE I.G., DOCHERRY K., TRUDEAU V.L.;			
RT	"Multiplication of glutamic acid decarboxylases (GAD) in vertebrates:			
RT	molecular phylogeny and evidence for a new GAD paralog."			
RL	Mol. Biol. Evol. 16:397-404(1999).			
DR	EMBL; AF043272; AAD22718.1;			
KW	Lyase.			
FT	NON TER			
FT	NON TER			
SO	SEQUENCE	182 AA; 19942 MW; 1699125D CRC32;		

Query Match 95.6%; Score 152; DB 13; Length 182;  
Best Local Similarity 95.0%; Pred. No. 1.86e-17;  
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

DB	38	SNMYAMMIARFKMFPEVK 57
Qy	1	SNMYAMMIARFKMFPEVK 20

RESULT 2  
AC 09W659; PRELIMINARY; PRT: 182 AA.  
DT 01-NOV-1999 (TREMBLrel. 12, Created)  
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)  
DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)  
DE GLUTAMATE DECARBOXYLASE ISOFORM 65 (EC 4.1.1.15) (FRAGMENT).  
GN GAD65.  
OS Psephenus guttata (zebra finch) (Taeniopygia guttata).

```

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;
OC Neognathae; Passeriformes; Estrildidae; Estrilidae; Taeniopygia.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RX MEDLINE: 99261650.
RA BOSMA P.T., BLAZQUEZ M., COLLINS M.A., BISHOP J.D.D., DROUIN G.,
  PRIDE I.G., DOCHERTY K., TRUDEAU V.L.;
RT "Multiplicity of glutamic acid decarboxylases (GAD) in vertebrates:
  molecular phylogeny and evidence for a new GAD paralog.";
RL Mol. Biol. Evol. 16:397-404(1999).
DR EMBL: AF043270; AAD22716.1; -.
KW Lyase.
FT NON_TER 1
FT NON_TER 182
SQ SEQUENCE 182 AA; 19918 MW; B67E4ADF CRC32;

Query Match 95.6%; Score 152; DB 13; Length 182;
Best Local Similarity 95.0%; Pred. No. 1,86e-17;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

DB 38 SNMYAMMLARFKMPEVK 57
QY 1 SNMYAMMLARFKMPEVK 20

RESULT 3
ID 09W654 PRELIMINARY; PRT; 182 AA.
AC 09W654:
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DE 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
DE GLUTAMATE DECARBOXYLASE ISOFORM 65 (EC 4.1.1.15) (FRAGMENT).
GN GAD65.
OS Carassius auratus (Goldfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
OC Neopterygii; Teleostei; Euteleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Cyprinidae; Cyprinidae; Carassius.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RX MEDLINE: 99261650.
RA BOSMA P.T., BLAZQUEZ M., COLLINS M.A., BISHOP J.D.D., DROUIN G.,
  PRIDE I.G., DOCHERTY K., TRUDEAU V.L.;
RT "Multiplicity of glutamic acid decarboxylases (GAD) in vertebrates:
  molecular phylogeny and evidence for a new GAD paralog.";
RL Mol. Biol. Evol. 16:397-404(1999).
DR EMBL: AF043265; AAD22711.1; -.
KW Lyase.
FT NON_TER 1
FT NON_TER 182
SQ SEQUENCE 182 AA; 20097 MW; A4A23079 CRC32;

Query Match 89.9%; Score 143; DB 13; Length 182;
Best Local Similarity 85.0%; Pred. No. 1,92e-15;
Matches 17; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

DB 38 SNMYAMMLARFKMPEVK 57
QY 1 SNMYAMMLARFKMPEVK 20

RESULT 4
ID 093275 PRELIMINARY; PRT; 232 AA.
AC 093275:
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
DE GLUTAMATE DECARBOXYLASE (EC 4.1.1.15) (FRAGMENT).
GN GAD5.
OS Brachydanio rerio (Zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
OC Neopterygii; Teleostei; Euteleostei; Ostariophysi; Cypriniformes;

```

```

OC Cyprinidae; Cyprinidae; Rasbora; Danio.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 98295903.
RA MARTIN S.C., HEINRICH G., SANDELL J.H.;
RT "Sequence and expression of glutamic acid decarboxylase isoforms in
  the developing zebrafish.";
RL J. Comp. Neurol. 396:253-266(1998).
CC -1- COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO GROUP II DECARBOXYLASES (DDC, GAD, HDC AND
  TYDC).
DR EMBL: AF017265; AAC24326.1; -.
DR PROSITE: PS00392; DDC_GAD_HDC_YDC; 1.
DR PFAM: PF00282; Pyridoxal-dec; 1.
KW Lyase; Decarboxylase; Pyridoxal phosphate.
FT NON_TER 1
FT NON_TER 232
SQ SEQUENCE 232 AA; 26059 MW; FD2B274F CRC32;

Query Match 89.9%; Score 143; DB 13; Length 232;
Best Local Similarity 85.0%; Pred. No. 1,92e-15;
Matches 17; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

DB 42 SNMYAMMLARFKMPEVK 61
QY 1 SNMYAMMLARFKMPEVK 20

RESULT 5
ID 09W656 PRELIMINARY; PRT; 182 AA.
AC 09W656:
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DE 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
DE GLUTAMATE DECARBOXYLASE ISOFORM 65 (EC 4.1.1.15) (FRAGMENT).
GN GAD5.
OS Coryphaenoides armatus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
OC Neopterygii; Teleostei; Euteleostei; Paracanthopterygii; Gadiformes;
OC Macrouridae; Coryphaenoides.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RX MEDLINE: 99261650.
RA BOSMA P.T., BLAZQUEZ M., COLLINS M.A., BISHOP J.D.D., DROUIN G.,
  PRIDE I.G., DOCHERTY K., TRUDEAU V.L.;
RT "Multiplicity of glutamic acid decarboxylases (GAD) in vertebrates:
  molecular phylogeny and evidence for a new GAD paralog.";
RL Mol. Biol. Evol. 16:397-404(1999).
DR EMBL: AF043267; AAD22713.1; -.
KW Lyase.
FT NON_TER 1
FT NON_TER 182
SQ SEQUENCE 182 AA; 19768 MW; 1225481D CRC32;

Query Match 86.8%; Score 138; DB 13; Length 182;
Best Local Similarity 85.0%; Pred. No. 2,46e-14;
Matches 17; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

DB 38 SNMYAMMLARFKMPEVK 57
QY 1 SNMYAMMLARFKMPEVK 20

RESULT 6
ID 09W657 PRELIMINARY; PRT; 182 AA.
AC 09W657:
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
DE GLUTAMATE DECARBOXYLASE ISOFORM 67 (EC 4.1.1.15) (FRAGMENT).
GN GAD5.
OS Coryphaenoides armatus.

```

Query Match	Best Local	Similarity	Score	DB	Length
Matches 14;	Conservative 4;	Mismatches 2;	Indels 0;	Gaps 0;	
<p>Db 42 SNMYSVMARYKYPPEVYKTK 61                : : : : : : :             QY 1 SNMYAMMIARFKMPPEVKEK 20</p>					
<p>RESULT 9 PRELIMINARY; PRT; 182 AA.</p>					
ID Q9W660;	AC Q9W660;	01-NOV-1999 (TREMBlrel. 12, Created)			
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)					
DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)					
DE GLUTAMATE DECARBOXYLASE ISOFORM 67 (EC 4.1.1.15) (FRAGMENT).					
GN GAD67.					
OS Pooephila guttata (Zebra finch) (Taeniopygia guttata).					
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Archosauria; Aves;					
OC Neognathae; Passeriformes; Estrilidae; Estrilidae; Taeniopygia.					
RN [1]					
RP SEQUENCE FROM N.A.					
RC TISSUE-BRAIN;					
RC MEDLINE; 99261650.					
RA BOSMA P.T., BLAZQUEZ M., COLLINS M.A., BISHOP J.D.D., DROUIN G.,					
RA PRIEDE I.G., DOCHERTY K., TRUDEAU V.L.;					
RT "Multiplicity of glutamic acid decarboxylases (GAD) in vertebrates:					
RT Molecular phylogeny and evidence for a new GAD paralogue."					
RL Mol. Biol. Evol. 16:397-404(1999).					
DR EMBL; AF043271; AAD22717.1; -					
KW Lyase.					
FT NON_TER 1					
FT NON_TER 182					
SO SEQUENCE 182 AA; 20057 MW; 721DBDF CRC32;					
<p>Query Match 70.4%; Score 112; DB 13; Length 182;            Best Local Similarity 70.0%; Pred. No. 9.33e-09;            Matches 14; Conservative 3; Mismatches 3; Indels 0; Gaps 0;</p>					
<p>Db 38 SNMYSIMARYKYPPEVYKTK 57                : : : : : : :             QY 1 SNMYAMMIARFKMPPEVKEK 20</p>					
<p>RESULT 10 PRELIMINARY; PRT; 182 AA.</p>					
ID Q9W663;	AC Q9W663;	01-NOV-1999 (TREMBlrel. 12, Created)			
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)					
DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)					
DE GLUTAMATE DECARBOXYLASE ISOFORM 67 (EC 4.1.1.15) (FRAGMENT).					
GN GAD67.					
OS Pseudemys scripta (Slider turtle)					

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Testudines;  
 OC Cryptodira; Testudinoidea; Emydidae; Trachemys.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-BRAIN;  
 RX MEDLINE; 99261650.  
 RA BOSMA P.T., BLAZQUEZ M., COLLINS M.A., BISHOP J.D.D., DROUIN G.,  
 PRIEDE I.G., DOHERTY K., TRUDEAU V.L.;  
 RT "Multiplicity of glutamic acid decarboxylases (GAD) in vertebrates:  
 molecular phylogeny and evidence for a new GAD paralog."  
 RL Mol. Biol. Evol. 16:397-404(1999).  
 DR EMBL; AF043274; AAD22720.1; -.  
 KW Lyase.  
 FT NON\_TER  
 SQ SEQUENCE 182 AA; 20047 MW; 002023C1 CRC32;  
 Query Match 70.4%; Score 112; DB 13; Length 182;  
 Best Local Similarity 70.0%; Pred. No. 9.32e-09;  
 Matches 14; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Db 38 SNMYSIMARKYFPEVKTK 57  
 ||||:||||:||||:  
 QY 1 SNMYSIMARKYFPEVKTK 20

RESULT 11  
 ID 091644 PRELIMINARY; PRT; 563 AA.  
 AC 091644;  
 DT 01-NOV-1996 (TREMBlrel. 01, Created)  
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
 DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)  
 DE GLUTAMIC ACID DECARBOXYLASE.  
 GN GAD.  
 OS Xenopus laevis (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Amphibia;  
 OC Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae; Xenopodinae;  
 OC Xenopus.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA WART S.D., SPITZER N.C.;  
 RL Submitted (OCT-1995) to the EMBL/GenBank/DBJ databases.  
 CC -1- COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY)  
 CC -1- SIMILARITY: BELONGS TO GROUP II DECARBOXYLASES (DDC, GAD, HDC AND  
 CC TYRDC).  
 DR EMBL; U38225; AAA96273.1; -.  
 DR PROSITE; PS00392; DDC\_GAD\_HDC\_YDC; 1.  
 DR PFAM; PF00282; Pyridoxal dec. 1.  
 KW Lyase; Decarboxylase; Pyridoxal phosphate.  
 SQ SEQUENCE 563 AA; 64095 MW; CBBB0C98 CRC32;

Query Match 70.4%; Score 112; DB 13; Length 563;  
 Best Local Similarity 70.0%; Pred. No. 9.32e-09;  
 Matches 14; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Db 224 SNMYSIMARKYFPEVKTK 243  
 ||||:||||:||||:  
 QY 1 SNMYSIMARKYFPEVKTK 20

RESULT 12  
 ID 09158 PRELIMINARY; PRT; 590 AA.  
 AC 09158;  
 DT 01-MAY-1999 (TREMBlrel. 10, Created)  
 DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)  
 DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)  
 DE GLUTAMATE DECARBOXYLASE 67.  
 GN GAD67.  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;  
 OC Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.  
 RN [1]  
 RP SEQUENCE FROM N.A.

RC STRAIN-WHITE LESHORN;  
 RA WAGBERG F.;  
 RT "Characterization of glutamate decarboxylase in chicken."  
 RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.  
 CC -1- COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO GROUP II DECARBOXYLASES (DDC, GAD, HDC AND  
 CC TYRDC).  
 DR EMBL; AF030355; AAD01902.1; -.  
 DR PROSITE; PS00392; DDC\_GAD\_HDC\_YDC; 1.  
 KW Lyase; Decarboxylase; Pyridoxal phosphate.  
 SQ SEQUENCE 590 AA; 66710 MW; 80B66DEF CRC32;  
 Query Match 70.4%; Score 112; DB 13; Length 590;  
 Best Local Similarity 70.0%; Pred. No. 9.32e-09;  
 Matches 14; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Db 251 SNMYSIMARKYFPEVKTK 270  
 ||||:||||:||||:  
 QY 1 SNMYSIMARKYFPEVKTK 20

RESULT 13  
 ID 008685 PRELIMINARY; PRT; 593 AA.  
 AC 008685;  
 DT 01-JUL-1997 (TREMBlrel. 04, Created)  
 DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update)  
 DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)  
 DE 67KD GLUTAMIC ACID DECARBOXYLASE.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 OC Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA STRAIN-BALB/C;  
 RA AUGT G., STEINBRENNER H., THAMM B., ROST A.K., SEISSLER J.;  
 RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.  
 CC -1- COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO GROUP II DECARBOXYLASES (DDC, GAD, HDC AND  
 CC TYRDC).  
 DR EMBL; Y12257; CAA72934.1; -.  
 DR PROSITE; PS00392; DDC\_GAD\_HDC\_YDC; 1.  
 DR PFAM; PF00282; Pyridoxal dec. 1.  
 KW Lyase; Decarboxylase; Pyridoxal phosphate.  
 SQ SEQUENCE 593 AA; 66648 MW; BAF92E0 CRC32;

Query Match 70.4%; Score 112; DB 11; Length 593;  
 Best Local Similarity 70.0%; Pred. No. 9.32e-09;  
 Matches 14; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Db 254 SNMYSIMARKYFPEVKTK 273  
 ||||:||||:||||:  
 QY 1 SNMYSIMARKYFPEVKTK 20

RESULT 14  
 ID 09W658 PRELIMINARY; PRT; 182 AA.  
 AC 09W658;  
 DT 01-NOV-1999 (TREMBlrel. 12, Created)  
 DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)  
 DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)  
 DE GLUTAMATE DECARBOXYLASE ISOFORM 3 (EC 4.1.1.15) (FRAGMENT).  
 GN GAD3.  
 OS Coryphaenoides armatus.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;  
 OC Neopterygii; Teleostei; Euteleostei; Paracanthopterygii; Gadiformes;  
 OC Macrouridae; Coryphaenoides.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-BRAIN;  
 RX MEDLINE; 99261650.  
 RA BOSMA P.T., BLAZQUEZ M., COLLINS M.A., BISHOP J.D.D., DROUIN G.,  
 PRIEDE I.G., DOHERTY K., TRUDEAU V.L.;  
 RT "Multiplicity of glutamic acid decarboxylases (GAD) in vertebrates:"



EMBL: AF043269. AAD22715.1 - molecular phylogeny and evidence for a new GAD paralog. *Mol. Biol. Evol.* 16:397-404(1999).

1	NON_TER	1	1
1	NON_TER	182	182
2	SEQUENCE	182 AA;	19812 MW; 30183853 CRC32

Query Match	67.38;	Score 107;	DB 13;	Length 182;
Best Local Similarity	50.08;	Pred. No. 1.00e-07;		
Matches	10;	Conservative	8;	Mismatches 2; Indels 0; Gaps 0

38 SNLYSMLVARYALYPDVKTK 57  
||:|:|:|:|:|:|:|:|:|  
1 SNMYAMMIARFKMFPEVKEK 20

RESULT	15
Q64577	
Q64577	
Q64577	
PRELIMINARY;	PRT;
	478 AA

1  
2  
3  
4  
5  
6  
7  
8  
9  
10  
11  
12  
13  
14  
15  
16  
17  
18  
19  
20  
21  
22  
23  
24  
25  
26  
27  
28  
29  
30  
31  
32  
33  
34  
35  
36  
37  
38  
39  
40  
41  
42  
43  
44  
45  
46  
47  
48  
49  
50  
51  
52  
53  
54  
55  
56  
57  
58  
59  
60  
61  
62  
63  
64  
65  
66  
67  
68  
69  
70  
71  
72  
73  
74  
75  
76  
77  
78  
79  
80  
81  
82  
83  
84  
85  
86  
87  
88  
89  
90  
91  
92  
93  
94  
95  
96  
97  
98  
99  
100  
101  
102  
103  
104  
105  
106  
107  
108  
109  
110  
111  
112  
113  
114  
115  
116  
117  
118  
119  
120  
121  
122  
123  
124  
125  
126  
127  
128  
129  
130  
131  
132  
133  
134  
135  
136  
137  
138  
139  
140  
141  
142  
143  
144  
145  
146  
147  
148  
149  
150  
151  
152  
153  
154  
155  
156  
157  
158  
159  
160  
161  
162  
163  
164  
165  
166  
167  
168  
169  
170  
171  
172  
173  
174  
175  
176  
177  
178  
179  
180  
181  
182  
183  
184  
185  
186  
187  
188  
189  
190  
191  
192  
193  
194  
195  
196  
197  
198  
199  
200  
201  
202  
203  
204  
205  
206  
207  
208  
209  
210  
211  
212  
213  
214  
215  
216  
217  
218  
219  
220  
221  
222  
223  
224  
225  
226  
227  
228  
229  
230  
231  
232  
233  
234  
235  
236  
237  
238  
239  
240  
241  
242  
243  
244  
245  
246  
247  
248  
249  
250  
251  
252  
253  
254  
255  
256  
257  
258  
259  
260  
261  
262  
263  
264  
265  
266  
267  
268  
269  
270  
271  
272  
273  
274  
275  
276  
277  
278  
279  
280  
281  
282  
283  
284  
285  
286  
287  
288  
289  
290  
291  
292  
293  
294  
295  
296  
297  
298  
299  
300  
301  
302  
303  
304  
305  
306  
307  
308  
309  
310  
311  
312  
313  
314  
315  
316  
317  
318  
319  
320  
321  
322  
323  
324  
325  
326  
327  
328  
329  
330  
331  
332  
333  
334  
335  
336  
337  
338  
339  
340  
341  
342  
343  
344  
345  
346  
347  
348  
349  
350  
351  
352  
353  
354  
355  
356  
357  
358  
359  
360  
361  
362  
363  
364  
365  
366  
367  
368  
369  
370  
371  
372  
373  
374  
375  
376  
377  
378  
379  
380  
381  
382  
383  
384  
385  
386  
387  
388  
389  
390  
391  
392  
393  
394  
395  
396  
397  
398  
399  
400  
401  
402  
403  
404  
405  
406  
407  
408  
409  
410  
411  
412  
413  
414  
415  
416  
417  
418  
419  
420  
421  
422  
423  
424  
425  
426  
427  
428  
429  
430  
431  
432  
433  
434  
435  
436  
437  
438  
439  
440  
441  
442  
443  
444  
445  
446  
447  
448  
449  
450  
451  
452  
453  
454  
455  
456  
457  
458  
459  
460  
461  
462  
463  
464  
465  
466  
467  
468  
469  
470  
471  
472  
473  
474  
475  
476  
477  
478  
479  
480  
481  
482  
483  
484  
485  
486  
487  
488  
489  
490  
491  
492  
493  
494  
495  
496  
497  
498  
499  
500  
501  
502  
503  
504  
505  
506  
507  
508  
509  
510  
511  
512  
513  
514  
515  
516  
517  
518  
519  
520  
521  
522  
523  
524  
525  
526  
527  
528  
529  
530  
531  
532  
533  
534  
535  
536  
537  
538  
539  
540  
541  
542  
543  
544  
545  
546  
547  
548  
549  
550  
551  
552  
553  
554  
555  
556  
557  
558  
559  
560  
561  
562  
563  
564  
565  
566  
567  
568  
569  
570  
571  
572  
573  
574  
575  
576  
577  
578  
579  
580  
581  
582  
583  
584  
585  
586  
587  
588  
589  
590  
591  
592  
593  
594  
595  
596  
597  
598  
599  
600  
601  
602  
603  
604  
605  
606  
607  
608  
609  
610  
611  
612  
613  
614  
615  
616  
617  
618  
619  
620  
621  
622  
623  
624  
625  
626  
627  
628  
629  
630  
631  
632  
633  
634  
635  
636  
637  
638  
639  
640  
641  
642  
643  
644  
645  
646  
647  
648  
649  
650  
651  
652  
653  
654  
655  
656  
657  
658  
659  
660  
661  
662  
663  
664  
665  
666  
667  
668  
669  
670  
671  
672  
673  
674  
675  
676  
677  
678  
679  
680  
681  
682  
683  
684  
685  
686  
687  
688  
689  
690  
691  
692  
693  
694  
695  
696  
697  
698  
699  
700  
701  
702  
703  
704  
705  
706  
707  
708  
709  
710  
711  
712  
713  
714  
715  
716  
717  
718  
719  
720  
721  
722  
723  
724  
725  
726  
727  
728  
729  
730  
731  
732  
733  
734  
735  
736  
737  
738  
739  
740  
741  
742  
743  
744  
745  
746  
747  
748  
749  
750  
751  
752  
753  
754  
755  
756  
757  
758  
759  
760  
761  
762  
763  
764  
765  
766  
767  
768  
769  
770  
771  
772  
773  
774  
775  
776  
777  
778  
779  
780  
781  
782  
783  
784  
785  
786  
787  
788  
789  
790  
791  
792  
793  
794  
795  
796  
797  
798  
799  
800  
801  
802  
803  
804  
805  
806  
807  
808  
809  
810  
811  
812  
813  
814  
815  
816  
817  
818  
819  
820  
821  
822  
823  
824  
825  
826  
827  
828  
829  
830  
831  
832  
833  
834  
835  
836  
837  
838  
839  
840  
84

Query Match	57.2%	Score 91;	DB 11;	Length 478;
Best Local Similarity	50.0%;	Pred. No. 1.54e-04;		
Matches	10; Conservative	6;	Mismatches 4;	Indels 0; Gaps 0

```

155 SNMYAINLARFORYPDCKOR 174
      |||||: :||| :|: |:|:
1 SNMYAMMIARFKMFPEVKEK 20

```

Search completed: Tue Mar 7 21:15:23 2000  
Job time : 9 secs.

**THIS PAGE BLANK (USPTO)**

\*\*\*\*\*  
Release 3.1A John F. Collins, Biocomputing Research Unit.  
Copyright (c) 1993-1998 University of Edinburgh, U.K.  
Distribution rights by Oxford Molecular Ltd  
\*\*\*\*\*

(TM)

MPsrch\_dp protein - protein database search, using Smith-Waterman algorithm  
Run on: Tue Mar 7 21:26:23 2000; MasPar time 3.91 Seconds  
121.227 Million cell updates/sec  
Tabular output not generated.

Title: >US-08-981-824-3  
(1-20) from US08981824.pep  
Description: 134  
Perfect Score: 134  
Sequence: 1 NWEIADQPONLEIIMHCOT 20

Scoring table: PAM 150  
Gap 15

Searched: 188965 segs, 23686106 residues

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: a-geneseq35  
1:geneseqp

Statistics: Mean 21.001; Variance 73.034; scale 0.288

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	154	100.0	20	1 W01795	Human 65 kD glutamine	1.92e-08
2	154	100.0	20	1 W18844	65 kD glutamic acid de	1.92e-08
3	154	100.0	503	1 R23645	Human GAD65 gene produ	1.92e-08
4	154	100.0	540	1 R59520	GAD65 1-45 N-terminal	1.92e-08
5	154	100.0	544	1 R59524	GAD65 545-585 C-termi	1.92e-08
6	154	100.0	554	1 R59518	GAD65 1-31 deleted, C4	1.92e-08
7	154	100.0	584	1 W86017	Human GAD65 protein se	1.92e-08
8	154	100.0	584	1 W34519	Human GAD65 protein	1.92e-08
9	154	100.0	585	1 W12402	65 kD human glutamic a	1.92e-08
10	154	100.0	585	1 W14915	Modified glutamic acid	1.92e-08
11	154	100.0	585	1 R28756	Human pancreatic islet	1.92e-08
12	154	100.0	585	1 R59516	Human GAD65	1.92e-08
13	154	100.0	585	1 R79105	Human glutamic acid de	1.92e-08
14	154	100.0	585	1 W14916	Modified glutamic acid	1.92e-08
15	154	100.0	585	1 R29629	Human GAD 65	1.92e-08
16	154	100.0	585	1 R29629	Human GAD 65	1.92e-08
17	154	100.0	585	1 W35361	Human 65K-glutamic aci	1.92e-08
18	142	92.2	540	1 R59521	GAD65 1-45 N-terminal	4.06e-07
19	142	92.2	544	1 R59525	GAD65 545-585 C-termi	4.06e-07
20	142	92.2	554	1 R59519	GAD65 1-31 deleted, C4	4.06e-07
21	142	92.2	584	1 W86018	Rat GAD65 protein sequ	4.06e-07
22	142	92.2	584	1 W34520	Rat GAD65 protein	4.06e-07
23	142	92.2	585	1 R23644	Rat GAD65 gene product	4.06e-07

ID	Score	Query Match	Length	ID	Description	Pred. No.
24	142	92.2	585	1 R29628	Rat GAD 65	4.06e-07
25	142	92.2	585	1 R59517	Rat GAD65	4.06e-07
26	142	92.2	605	1 R71733	Rat glutamic acid deca	4.06e-07
27	120	77.9	22	1 R72270	Glutamic acid decarbox	9.95e-05
28	86	55.8	593	1 R27220	Brain GAD #2	3.49e-01
29	86	55.8	594	1 R27222	Full length islet GAD	3.49e-01
30	86	55.8	594	1 W74717	Amino acid sequence of	3.49e-01
31	86	55.8	594	1 R27221	Full length brain GAD	3.49e-01
32	86	55.8	594	1 W74716	Amino acid sequence of	3.49e-01
33	82	53.2	368	1 W99093	Rhodospiridium torula	8.76e-01
34	82	53.2	368	1 W31362	R. gracilis D-amino ac	8.76e-01
35	72	45.8	20	1 R10976	Glutamic acid decarbox	8.35e+00
36	63	40.9	429	1 R10976	Polyhydroxyalkanoate p	5.30e+01
37	61	39.6	483	1 W31338	Amino acid sequence of	9.01e+01
38	60	39.0	663	1 W09055	Nicotiana glauca	1.11e+02
39	60	39.0	666	1 R75366	Adhesin	1.11e+02
40	58	37.7	152	1 Y07969	Human secreted protein	1.68e+02
41	58	37.7	357	1 W85465	Secreted protein encod	1.68e+02
42	58	37.7	748	1 W03174	Mouse STAT	1.68e+02
43	58	37.7	748	1 R72081	Mouse Stat (13stl)	1.68e+02
44	58	37.7	3587	1 R34713	Bacillus subtilis srfA	1.68e+02
45	58	37.7	3588	1 R34712	Bacillus subtilis srfA	1.68e+02

## ALIGNMENTS

RESULT 1  
ID W01795 standard; peptide: 20 AA.  
AC W01795 standard; peptide: 20 AA.

DE Human-65 kD glutamine decarboxylase peptide.  
KW Human: glutamine decarboxylase; GAD; diagnosis: predisposition;

KW tumour; immunological; disease; autoimmune; diabetes; reagent;

KW determination; T cell; subpopulation; medicament; treatment;

KW prevention; production; antigen; immunogen; tolerogen; isolation;

KW reinjection; inactivation.

OS Homo sapiens.

PN DE19525784-AI.

PD 16-JAN-1997.

PF 14-JUL-1995; 025784.

PR 14-JUL-1995; DE-025784.

PA (BOEF) BOEHRINGER MANNHEIM GMBH.

PI Albert W, Boltard C, Endl J, Jung G, Schendel D;

PI Stahl P, Van Ender P;

DR WPI: 97-078452/08.

PT Glutamine decarboxylase peptide(s) - for diagnosis and therapy of

PT diabetes, etc.

PS Claim 1; Page 12; 15pp; German.

CC The present peptide is a fragment of the human 65 kD glutamine

CC decarboxylase (GAD), which can be used to diagnose, or diagnose a

CC predisposition to, a tumour or immunological disease, preferably an

CC autoimmune disease, especially diabetes. It can also be used as a

CC reagent to determine specific T cell subpopulations, in medicaments

CC to treat or prevent immunological diseases, preferably autoimmune

CC diseases, especially diabetes, to produce antigens, especially

CC immunogens or tolerogens and to isolate specific T cell

CC subpopulations, which can be used to produce antigens or for

CC reinjection, optionally after inactivation.

Sequence 20 AA:

Query Match 100.0%; Score 154; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 1.92e-08;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 1 NWEIADQPONLEIIMHCOT 20

OY 1 NWEIADQPONLEIIMHCOT 20

RESULT 2

ID W18844 standard; peptide: 20 AA.

AC W18844 standard; peptide: 20 AA.

DT 05-JAN-1998 (first entry)

DE 65 kD glutamic acid decarboxylase peptide fragment III.  
KW GAD: 65 kD: human; glutamic acid decarboxylase; autoreactive; diagnosis;  
KW insulin-dependent diabetes mellitus; IDDM; cell-mediated disease;  
KW predilection; autoimmune; tumour; rheumatoid arthritis;  
KW multiple sclerosis  
OS Synthetic.  
PN DE19526561-A1.  
PD 23-JUN-1997.  
PF 20-JUL-1995; 026561.  
PR 20-JUL-1995; DE-026561.  
PA (BOER ) BOEHRINGER MANNHEIM GMBH.  
PI Donle F, Endl J, Ganz M, Jung G, Kientsch-engel R;  
PI Pozzilli P, Stahl P;  
DR WPI: 97-088254/09.  
PT Skin test for diagnosis of cell-mediated diseases, esp. diabetes -  
PT involving intradermal admin. of auto-reactive substances  
PS Claim 11: Page 9; 12pp: German.  
CC M18842-70 are peptide fragments of the 65 kD human glutamic acid  
CC decarboxylase (GAD). The fragments are autoreactive substances used for  
CC diagnosis of insulin-dependent diabetes mellitus (IDDM). The diagnosis is  
CC determined by using a claimed method for diagnosis of cell-mediated  
CC diseases or a predilection to cell-mediated diseases, which is effected  
CC by administering an autoreactive substance intradermally and establishing  
CC the diagnosis on the basis of the occurrence or lack of a positive  
CC reaction at the site of administration. The method is used for diagnosis  
CC of autoimmune and tumour diseases, preferably T-cell-mediated diseases  
CC such as rheumatoid arthritis, multiple sclerosis and especially IDDM.  
SQ Sequence 20 AA;

Query Match 100.0%; Score 154; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1,92e-08;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Dd 1 NMELADQPONLEIIMHCOT 20  
|||  
QY 1 NMELADQPONLEIIMHCOT 20

RESULT 3  
ID R23645 standard; Protein: 503 AA.

AC R23645;  
DT 02-NOV-1992 (first entry)  
DE Human GAD65 gene product.  
KW Glutamic acid decarboxylase; IDDM; stiff man syndrome;  
KW autoantibodies.  
OS Homo sapiens.  
PN WO9205446-A.  
PD 02-APR-1992.  
PF 23-SEP-1991; 006872.  
PR 21-SEP-1990; US-386336.  
PA (REGC ) UNIV CALIFORNIA.  
PA (REGC ) UNIV CALIFORNIA.  
PA (REGC ) UNIV OF CALIFORNIA.  
PI Erlander MG, Kaufman DL, Tobin AJ;  
DR WPI: 92-150489/18.  
DR N-PSDB; Q24184.  
PT Novel cDNA encoding GAD65 polypeptide - used to produce GAD65 for  
PT therapeutic and diagnostic application in insulin-dependent  
PT diabetes mellitus patients  
PS Disclosure: Fig 3; 53pp: English.  
CC The sequence given is a glutamic acid decarboxylase (GAD65). GAD65  
CC can be used for the diagnosis and therapy of patients with autoimmune  
CC diseases, esp. insulin-dependent diabetes mellitus (IDDM) and "stiff  
CC man" syndrome. It is possible to use either the entire GAD65 protein  
CC or polypeptide fragments of it for the immunological detection of  
CC autoantibodies to GAD65 which are indicative of IDDM and other auto-  
CC immune diseases. The production of this sequence by recombinant DNA  
CC technology allows large scale production of eukaryotic GAD65 in its  
CC native form without the need for separation from other proteinaceous  
CC prods.  
SQ Sequence 503 AA;

Query Match 100.0%; Score 154; DB 1; Length 503;

Best Local Similarity 100.0%; Pred. No. 1,92e-08;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Dd 146 NMELADQPONLEIIMHCOT 165  
|||  
QY 1 NMELADQPONLEIIMHCOT 20

RESULT 4  
ID R59520 standard; Protein: 540 AA.  
AC R59520;  
DT 09-NOV-1994 (first entry)  
DE GAD65 1-45 N-terminal-deleted mutant.  
KW GAD65; glutamate-decarboxylase; diabetes mellitus;  
KW stiff man syndrome; autoantibody; mutagenesis.  
OS Homo sapiens.  
PN WO9412529-A.  
PD 09-JUN-1994.  
PF 02-DEC-1993; U11705.  
PR 03-DEC-1992; US-984935.  
PA (REGC ) UNIV CALIFORNIA.  
PI Baekkeskov S, Kim J, Narnchuk M, Richter W, Shi Y;  
DR WPI: 94-200193/24.  
PT New soluble fragments of glutamic acid decarboxylase protein -  
PT used for the diagnosis and treatment of insulin dependent  
PT diabetes mellitus and stiff man syndrome.  
PS Disclosure: Fig. 1; 73pp: English.  
CC The amino acid sequences of human GAD65 (R59516) and rat GAD65  
CC (R59517) were determined. New soluble fragments of GAD65  
CC (R59518-25) were prepared by deletion/substitution  
CC mutagenesis. These fragments are free of N-terminal amino acids  
CC that limit solubility. Different fragments contain epitopes for  
CC different classes of GAD65 autoantibodies.  
SQ Sequence 540 AA;

Query Match 100.0%; Score 154; DB 1; Length 540;  
Best Local Similarity 100.0%; Pred. No. 1,92e-08;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Dd 101 NMELADQPONLEIIMHCOT 120  
|||  
QY 1 NMELADQPONLEIIMHCOT 20

RESULT 5  
ID R59524 standard; Protein: 544 AA.

AC R59524;  
DT 09-NOV-1994 (first entry)  
DE GAD65 545-585 C-terminal-deleted mutant.  
KW GAD65; glutamate-decarboxylase; diabetes mellitus;  
KW stiff man syndrome; autoantibody; mutagenesis.  
OS Homo sapiens.  
PN WO9412529-A.  
PD 09-JUN-1994.  
PF 02-DEC-1993; U11705.  
PR 03-DEC-1992; US-984935.  
PA (REGC ) UNIV CALIFORNIA.  
PI Baekkeskov S, Kim J, Narnchuk M, Richter W, Shi Y;  
DR WPI: 94-200193/24.  
PT New soluble fragments of glutamic acid decarboxylase protein -  
PT used for the diagnosis and treatment of insulin dependent  
PT diabetes mellitus and stiff man syndrome.  
PS Disclosure: Fig. 1; 73pp: English.  
CC The amino acid sequences of human GAD65 (R59516) and rat GAD65  
CC (R59517) were determined. New soluble fragments of GAD65  
CC (R59518-25) were prepared by deletion/substitution  
CC mutagenesis. The C-terminally deleted mutants given in R59524-25  
CC are able to recognize IDDM autoantibodies having the specificity  
CC of MIC4/MICA6, but not those having the specificity of MIC41/MICA3  
CC or MIC42. These mutants also have some N-terminal modifications  
CC to improve solubility.  
SQ Sequence 544 AA;

Query Match 100.0%; Score 154; DB 1; Length 544;  
 Best Local Similarity 100.0%; Pred. No. 1.92e-08;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 146 NWEIADOPNLEIIMHCOT 165  
 ||||||||||||||||  
 QY 1 NWEIADOPNLEIIMHCOT 20

RESULT 6  
 ID R59518 standard; protein; 554 AA.  
 AC R59518;  
 DT 09-NOV-1994 (first entry)  
 DE GAD65 1-31 deleted; C45A mutant.  
 KW GAD65; glutamate-decarboxylase; diabetes mellitus;  
 KM stiff man syndrome; autoantibody; mutagenesis.  
 OS Homo sapiens.  
 PN M09412529-A.  
 PD 09-JUN-1994.  
 PF 02-DEC-1993; U11705.  
 PR 03-DEC-1992; US-984935.  
 PA (REGC) UNIV CALIFORNIA.  
 PI Baekkeskov S, Kim J, Nanchuk M, Richter W, Shi Y;  
 DR WPI: 94-200193/24.  
 PT New soluble fragments of glutamic acid decarboxylase protein -  
 used for the diagnosis and treatment of insulin dependent  
 PT diabetes mellitus and stiff man syndrome.  
 PS Disclosure: Fig. 1; 73pp; English.  
 CC The amino acid sequences of human GAD65 (R59516) and rat GAD65  
 CC (R59517) were determined. New soluble fragments of GAD65  
 CC (R59518-25) were prepared by deletion/substitution  
 CC mutagenesis. These fragments are free of N-terminal amino acids  
 CC that limit solubility. Different fragments contain epitopes for  
 CC different classes of GAD65 autoantibodies.  
 SQ Sequence 554 AA;

Query Match 100.0%; Score 154; DB 1; Length 554;  
 Best Local Similarity 100.0%; Pred. No. 1.92e-08;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 115 NWEIADOPNLEIIMHCOT 134  
 ||||||||||||||||  
 QY 1 NWEIADOPNLEIIMHCOT 20

RESULT 7  
 ID W86017 standard; protein; 584 AA.  
 AC W86017;  
 DT 22-FEB-1999 (first entry)  
 DE Human GAD65 protein sequence.  
 KW GAD65; autoantibody; soluble; detection; diagnosis; monitor; IDDM;  
 KM insulin-dependent diabetes mellitus; stiff man syndrome.  
 OS Homo sapiens.  
 PN US5849506-A.  
 PD 15-DEC-1998.  
 PF 25-MAY-1993; 450755.  
 PR 02-DEC-1993; US-161290.  
 PR 03-DEC-1992; US-984935.  
 PR 25-MAY-1995; US-450755.  
 PA (REGC) UNIV CALIFORNIA.  
 PI Baekkeskov S, Kim J, Nanchuk M, Richter W, Shi Y;  
 DR WPI: 99-069120/06.  
 PT Immunoassay for GAD65 auto-antibodies - used for diagnosis of  
 PT diabetes and stiff man syndrome  
 PS Examples: Fig 1; 31pp; English.  
 CC This represents a human GAD65 protein sequence. The invention provides  
 CC soluble fragments of GAD65 that are specifically reactive with at least  
 CC one class of GAD65 autoantibody. The fragments are substantially free of  
 CC N-terminal amino acids that would otherwise limit solubility. Different  
 CC fragments contain different epitopes for different classes of GAD65  
 CC autoantibodies. These fragments are used in the methods of the invention  
 CC for detection of GAD65 autoantibodies. The methods are used for  
 CC diagnosing or monitoring insulin-dependent diabetes mellitus (IDDM) and

CC stiff man syndrome.  
 SQ Sequence 584 AA;

Query Match 100.0%; Score 154; DB 1; Length 584;  
 Best Local Similarity 100.0%; Pred. No. 1.92e-08;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 146 NWEIADOPNLEIIMHCOT 165  
 ||||||||||||||||  
 QY 1 NWEIADOPNLEIIMHCOT 20

RESULT 8  
 ID W34519 standard; protein; 584 AA.  
 AC W34519;  
 DT 24-MAR-1998 (first entry)  
 DE Human GAD65 protein.  
 KW GAD65; glutamic acid decarboxylase protein; human; soluble fragment;  
 KM autoantibody; insulin-dependent diabetes mellitus; IDDM; diagnosis;  
 KM stiff man syndrome; therapy.  
 OS Homo sapiens.  
 PN US5691448-A.  
 PD 25-NOV-1997.  
 PF 02-DEC-1993; 161290.  
 PR 02-DEC-1993; US-161290.  
 PR 03-DEC-1992; US-984935.  
 PA (BAEK/) BAEKESKOV S.  
 PA (KIM/) KIM J.  
 PA (NAMC/) NAMCHUK M.  
 PA (RICH/) RICHTER W.  
 PA (SHI/) SHI Y.  
 PI Baekkeskov S, Kim J, Nanchuk M, Richter W, Shi Y;  
 DR WPI: 98-017711/02.  
 PT Soluble fragments of glutamic acid decarboxylase GAD65 - used to  
 PT distinguish between insulin-dependent diabetes mellitus and  
 PT stiff-man syndrome  
 PS Disclosure: column 27-30; 30pp; English.  
 CC This sequence represents the human glutamic acid decarboxylase protein  
 CC GAD65. The invention relates to soluble fragments of a GAD65 protein that  
 CC are specifically reactive with a GAD65 autoantibody (AAb), where the  
 CC fragment is at least 99% pure and the AAb binds to a conformational  
 CC epitope of the fragment. The soluble GAD65 fragments can be used to  
 CC distinguish between insulin-dependent diabetes mellitus (IDDM) and stiff  
 CC man syndrome. They can also be used for diagnosis and treatment of IDDM  
 CC and stiff man syndrome. The fragments can distinguish different temporal  
 CC stages in the progression of IDDM.  
 SQ Sequence 584 AA;

Query Match 100.0%; Score 154; DB 1; Length 584;  
 Best Local Similarity 100.0%; Pred. No. 1.92e-08;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 146 NWEIADOPNLEIIMHCOT 165  
 ||||||||||||||||  
 QY 1 NWEIADOPNLEIIMHCOT 20

RESULT 9  
 ID W12402 standard; protein; 585 AA.  
 AC W12402;  
 DT 08-OCT-1997 (first entry)  
 DE 65 kD human glutamic acid decarboxylase isoform.  
 KW 65 kD glutamic acid decarboxylase; human; GAD65; enzyme; pancreas;  
 KM neuron; central nervous system; type I diabetes; autoimmune response;  
 KM T cell; therapy.  
 OS Homo sapiens.  
 PN W09700891-A1.  
 PD 09-JAN-1997.  
 PF 24-JUN-1996; U10790.  
 PR 23-JUN-1995; US-494624.  
 PA (KENN-) KENNEDY INST RHEUMATOLOGY.  
 PA (NEUR-) NEUROCRINE BIOSCIENCES INC.  
 PA (SBAR-) ST BARTHOLOMEW S HOSPITAL CENT CLINICAL.

PI Conlon PJ, Gaur A, Leslie RDG, Ling N, Londei M;  
 DR WPI: 97-087322/08.  
 DR N-PSDB: T61097.  
 PT New human glutamic acid decarboxylase peptide(s) - used for  
 PT treatment, diagnosis and determining predisposition to diabetes and  
 PT for ameliorating auto-immune responses.  
 PS Disclosure: Fig 1: 28pp; English.  
 CC This sequence represents the 65 kD isoform of human glutamic acid  
 CC decarboxylase (GAD65). GAD is an enzyme expressed in the beta cells of  
 CC the pancreas, and in neurons of the central nervous system. There are two  
 CC isoforms of GAD, a 67 kD isoform, and GAD65. Immunodominant regions of  
 CC GAD65 have been identified in Type I diabetic patients. Fragments of  
 CC GAD65, and analogues of the fragments, are used in the methods of the  
 CC invention. The methods are for detecting or treating diabetes or a  
 CC predisposition to diabetes. The peptides can also be used for  
 CC ameliorating an autoimmune response in a patient. Alteration of the  
 CC native peptides with selective changes of crucial residues can induce  
 CC unresponsiveness or change the responsiveness of antigen-specific  
 CC autoreactive T cells. The peptide analogues compete for binding to MHC  
 CC and do not cause proliferation of the corresponding native  
 CC peptide-specific T cells.  
 SQ Sequence 585 AA;

Query Match 100.0%; Score 154; DB 1; Length 585;  
 Best Local Similarity 100.0%; Pred. No. 1.92e-08;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 146 NWEIADQPONEIIMHCOT 165  
 ||||||||||||||||  
 QY 1 NWEIADQPONEIIMHCOT 20

RESULT 10  
 ID W14915 standard; Protein; 585 AA.  
 AC W14915;  
 DT 10-JUL-1997 (first entry)  
 DE Modified glutamic acid decarboxylase (K396R).  
 KW Glutamic acid decarboxylase; GAD; autoimmune disease; therapy;  
 KW insulin-dependent diabetes mellitus; vaccine;  
 KW enzyme engineering; protein engineering.  
 OS Synthetic.  
 PN WO9712034-A1.  
 PD 03-APR-1997.  
 PF 27-SEP-1996; SE1210.  
 PR 29-SEP-1995; SE-003379.  
 PA (SYNTE-) SYNECTICS BIOTECHNOLOGY AB.  
 PI Essen-Moeller A, Falorni A, Lernmark A, Robertson J;  
 DR WPI: 97-212895/19.  
 DR N-PSDB: T64560.  
 PT Modified glutamic acid decarboxylase for autoimmune disease  
 PT treatment - has immunoreactivity of unmodified GAD65 but decreased  
 PT enzyme activity, esp. useful for insulin-dependent diabetes mellitus  
 PT treatment  
 PS Claim 3: Page 13-15; 24pp; English.  
 CC A modified human glutamic acid decarboxylase (GAD) (W14915) has the  
 CC native lysine residue at amino acid position 356 replaced by  
 CC arginine. It is obcd. by site-directed mutagenesis (see also  
 CC T64561) of native human GAD65 cDNA and expression of the mutant DNA  
 CC (T64560) in transformed host cells. Lys-356 is critical for enzyme  
 CC activity. By replacing it with an amino acid incapable of Schiff  
 CC base formation, immunoreactivity is maintained but enzyme activity  
 CC is reduced or lost, so minimizing the risk of toxicity. The  
 CC modified GAD can be used to treat and/or prevent autoimmune  
 CC disorders such as insulin-dependent diabetes mellitus (IDDM) and  
 CC other diseases, e.g. neurological diseases, esp. in individuals  
 CC having a genetic predisposition for IDDM or with an increased  
 CC antibody titre against GAD.  
 SQ Sequence 585 AA;

Query Match 100.0%; Score 154; DB 1; Length 585;  
 Best Local Similarity 100.0%; Pred. No. 1.92e-08;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 146 NWEIADQPONEIIMHCOT 165  
 ||||||||||||||||  
 QY 1 NWEIADQPONEIIMHCOT 20

RESULT 11  
 ID R28756 standard; Protein; 585 AA.  
 AC R28756;  
 DT 20-APR-1993 (first entry)  
 DE Human pancreatic islet cell glutamic acid decarboxylase.  
 KW GAD; insulin dependent diabetes mellitus; IDDM; autoantibody detection.  
 OS Homo sapiens.  
 PN WO9220811-A.  
 PD 26-NOV-1992.  
 PF 14-MAY-1992; U04079.  
 PR 15-MAY-1991; US-702162.  
 PA (UNITW ) UNIV WASHINGTON.  
 PI (ZYMO ) ZYMOGENETICS INC.  
 PT Foster DC, Grubin CE, Hagopian W, Karlson AE, Lernmark A, Ohara PJ;  
 DR WPI: 92-415789/50.  
 DR N-PSDB: Q31783.  
 PT Polynucleotide encoding human islet glutamic acid decarboxylase -  
 PT used to test for auto-antibodies against itself to diagnose  
 PT insulin dependent diabetes mellitus  
 PS Disclosure: Fig 2: 45pp; English.  
 CC The sequence is that of human pancreatic islet glutamic acid  
 CC decarboxylase (GAD) which is used to test biological samples for  
 CC the presence of autoantibodies to human GAD. It can also be used  
 CC to remove antibodies against GAD from plasma in order to treat an  
 CC autoimmune response to GAD, e.g. in insulin-dependent diabetes mellitus  
 CC (IDDM), and may also be used to induce immunological tolerance to GAD  
 CC by giving GAD that specifically binds the GAD receptor on immature T  
 CC or B cells.  
 SQ Sequence 585 AA;

Query Match 100.0%; Score 154; DB 1; Length 585;  
 Best Local Similarity 100.0%; Pred. No. 1.92e-08;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 146 NWEIADQPONEIIMHCOT 165  
 ||||||||||||||||  
 QY 1 NWEIADQPONEIIMHCOT 20

RESULT 12  
 ID R59516 standard; Protein; 585 AA.  
 AC R59516;  
 DT 09-NOV-1994 (first entry)  
 DE Human GAD65.  
 KW GAD65; glutamate-decarboxylase; diabetes mellitus;  
 KW stiff man syndrome; autoantibody.  
 OS Homo sapiens.  
 PN WO9412529-A.  
 PD 09-JUN-1994.  
 PF 02-DEC-1993; U11705.  
 PR 03-DEC-1992; US-984935.  
 PA (RBGC ) UNIV CALIFORNIA.  
 PI Baekskov S, Kim J, Nanchuk M, Richter W, Shi Y;  
 DR WPI: 94-200193/24.  
 PT New soluble fragments of glutamic acid decarboxylase protein -  
 PT used for the diagnosis and treatment of insulin dependent  
 PT diabetes mellitus and stiff man syndrome.  
 PS Disclosure: Fig. 1: 73pp; English.  
 CC The amino acid sequences of human GAD65 (R59516) and rat GAD65  
 CC (R59517) were determined. New soluble fragments of GAD65  
 CC (R59518-25) were prepared by deletion/substitution  
 CC mutagenesis. These fragments are free of N-terminal amino acids  
 CC that limit solubility. Different fragments contain epitopes for  
 CC different classes of GAD65 autoantibodies.  
 SQ Sequence 585 AA;

Query Match 100.0%; Score 154; DB 1; Length 585;  
 Best Local Similarity 100.0%; Pred. No. 1.92e-08;

Matches 20: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 146 NWELADQPONLEIIMHCQT 165  
 |||||||  
 QY 1 NWELADQPONLEIIMHCQT 20

RESULT 13  
 ID R79105 standard; Protein: 585 AA.  
 AC R79105;  
 DT 13-NOV-1995 (first entry)  
 DE Human glutamic acid decarboxylase (GAD65).  
 KW Rat glutamic acid decarboxylase; GAD65; autoimmune disorders;  
 KM Insulin-dependent diabetes mellitus; stiff man disease.  
 OS Homo sapiens.  
 PN WO9507992-A.  
 PD 23-MAR-1995.  
 PF 24-AUG-1994; U09478.  
 PR 17-SEP-1993; US-123859.  
 PA (REGC ) UNIV CALIFORNIA.  
 PI Clare-Salzler MJ, Erlander MG, Kaufman DL, Tobin AJ;  
 DR MPI: 95-131360/17.  
 N-PSDB: Q86482.  
 PT New polypeptide fragments of glutamic acid decarboxylase - for  
 PT diagnosis and treatment of autoimmune disease, esp. insulin  
 PT dependent diabetes; also related nucleic acid, vectors,  
 PT antibodies, hydridoma(s) etc.  
 CC Example 1: Fig 3; 100bp; English.  
 CC Q86481 and Q86482 encode R71733 and R79105, rat and human glutamic  
 CC acid decarboxylase (GAD65) respectively, from which the GAD65  
 CC fragments described in R72261-R72298 were derived. These fragments  
 CC can be used to detect autoantibodies against GAD, e.g. to diagnose  
 CC and treat GAD-related autoimmune disorders, such as insulin  
 CC dependent diabetes mellitus or stiff man disease.  
 SQ Sequence 585 AA;

Query Match 100.0%; Score 154; DB 1; Length 585;  
 Best Local Similarity 100.0%; Pred. No. 1.92e-08;  
 Matches 20: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 146 NWELADQPONLEIIMHCQT 165  
 |||||||  
 QY 1 NWELADQPONLEIIMHCQT 20

RESULT 14  
 ID W14916 standard; Protein: 585 AA.  
 AC W14916;  
 DT 10-JUL-1997 (first entry)  
 DE Modified glutamic acid decarboxylase.  
 KW Glutamic acid decarboxylase; GAD; autoimmune disease; therapy;  
 KM Insulin-dependent diabetes mellitus; vaccine;  
 OS Synthetic.  
 FH Key Location/Qualifiers  
 FT msc-difference 396  
 FT /label= Ile, Arg, Gln, His, Gly  
 PN WO9712034-A1.  
 PD 03-APR-1997.  
 PF 27-SEP-1996; SFL1210.  
 PR 29-SEP-1995; SE-003379.  
 PA (SYNE-) SYNECTICS BIOTECHNOLOGY AB.  
 PI Essen-Moeller A, Falorni A, Lernmark A, Robertson J;  
 DR MPI: 97-212895/19.  
 PT Modified glutamic acid decarboxylase for autoimmune disease  
 PT treatment - has immunoreactivity of unmodified GAD65 but decreased  
 PT enzyme activity, esp. useful for insulin-dependent diabetes mellitus  
 PT treatment  
 PS Claim 1: Page 16-18; 24pp; English.  
 CC A modified human glutamic acid decarboxylase (GAD) (W14915) has the  
 CC native Lys residue at amino acid position 396 replaced by Ile, Gln,  
 CC His, Gly or esp. Arg (see also W14915). It is obtd. by site-  
 CC directed mutagenesis of native human GAD65 cDNA and expression of

CC the mutant DNA in transformed host cells. Lys-396 is critical for  
 CC enzyme activity. By replacing it with an amino acid incapable of  
 CC Schiff base formation, immunoreactivity is maintained but enzyme  
 CC activity is reduced or lost, so minimizing the risk of toxicity.  
 CC The modified GAD can be used to treat and/or prevent autoimmune  
 CC disorders such as insulin-dependent diabetes mellitus (IDDM) and  
 CC other diseases, e.g. neurological diseases, esp. in individuals  
 CC having a genetic predisposition for IDDM or with an increased  
 CC antibody titre against GAD.  
 SQ Sequence 585 AA;

Query Match 100.0%; Score 154; DB 1; Length 585;  
 Best Local Similarity 100.0%; Pred. No. 1.92e-08;  
 Matches 20: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 146 NWELADQPONLEIIMHCQT 165  
 |||||||  
 QY 1 NWELADQPONLEIIMHCQT 20

RESULT 15  
 ID R71641 standard; Protein: 585 AA.  
 AC R71641;  
 DT 21-SEP-1995 (first entry)  
 DE Human GAD.  
 KW GAD; glutamic-acid-decarboxylase; glutamate-decarboxylase;  
 KM non-insulin-dependent diabetes; NIDDM; diagnosis; autoantibody;  
 KW pancreas; islet.  
 OS Homo sapiens.  
 FH Key Location/Qualifiers  
 FT binding-site 394..399  
 FT /label= Pyridoxal-5'-phosphate-binding-site  
 PN WO9507464-A.  
 PD 16-MAR-1995.  
 PF 02-SEP-1994; U09937.  
 PR 07-SEP-1993; US-117907.  
 PA (UNITV ) UNIV WASHINGTON.  
 PI Hagopian W, Karlisen AE, Landin-Olsson M, Lernmark A;  
 DR MPI: 95-123512/16.  
 N-PSDB: Q86046.  
 PT Predicting the clinical course of diabetes in patients with  
 PT non-insulin dependent diabetes mellitus - by detecting the  
 PT presence of autoantibodies to human islet glutamic acid  
 PT decarboxylase.  
 PS Claim 8: Page 40-44; 62pp; English.  
 CC A human islet cDNA library was screened for colonies containing  
 CC GAD cDNA using probes (given in Q86047-49) based on conserved  
 CC internal and N- and C-terminal regions of cat, rat and mouse brain  
 CC GAD. Full-length clones were obtained by PCR-RACE. The entire  
 CC sequence of the human islet GAD cDNA is given in Q86046 and the  
 CC encoded protein in R71641. GAD was used to screen sera for the  
 CC presence of GAD autoantibodies.  
 SQ Sequence 585 AA;

Query Match 100.0%; Score 154; DB 1; Length 585;  
 Best Local Similarity 100.0%; Pred. No. 1.92e-08;  
 Matches 20: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 146 NWELADQPONLEIIMHCQT 165  
 |||||||  
 QY 1 NWELADQPONLEIIMHCQT 20

Search completed: Tue Mar 7 21:26:31 2000  
 Job time : 8 secs.

**THIS PAGE BLANK (USPTO)**





```

Kaufman, D.L.; Wagner-McPherson, C.B.; Evans, G.A.; Tobin,
A.J.
#journal Proc. Natl. Acad. Sci. U.S.A. (1992) 89:2115-2119
#title Two human glutamate decarboxylases, 65-kDa GAD and 67-kDa
#cross-references MUID:92196068
#accession A41935
##molecule_type mRNA
##residues 1-585 ##label BU1
##cross-references GB:M81882; NID:g182933; PIDN:AAA62367.1; PID:g182934
##experimental_source brain
#note sequence extracted from NCBI backbone (NCBIP:88007)
REFERENCE
#authors Karlsten, A.E.; Hagopian, W.A.; Grubin, C.E.; Dube, S.;
Disteche, C.M.; Adler, D.A.; Baetmeier, H.; Mathewes, S.;
Grant, F.J.; Foster, D.; Lermarck, A.
#journal Proc. Natl. Acad. Sci. U.S.A. (1991) 88:8337-8341
#title Cloning and primary structure of a human islet isoform of
glutamic acid decarboxylase from chromosome 10.
#cross-references MUID:92020848
#accession A41292
##molecule_type mRNA
##residues 1-585 ##label KAR
##cross-references GB:M74826; NID:g182931; PIDN:AAA58491.1; PID:g182932
##experimental_source pancreatic islet
REFERENCE
#authors Mauch, L.; Abney, C.C.; Berg, H.; Scherbaum, W.A.; Liedvogel,
B.; Northemann, W.
#journal Eur. J. Biochem. (1993) 212:597-603
#title Characterization of a linear epitope within the human
pancreatic 64-kDa glutamic acid decarboxylase and its
autoimmune recognition by sera from insulin-dependent
diabetes mellitus patients.
#cross-references MUID:93185681
#accession S30058
##molecule_type mRNA
##residues 6-585 ##label MAU
##cross-references EMBL:X69936
##experimental_source pancreatic islet
REFERENCE
#authors Bu, D.F.; Tobin, A.J.
#journal Genomics (1994) 21:222-228
#title The exon-intron organization of the genes (GAD1 and GAD2)
encoding two human glutamate decarboxylases (GAD-67 and
GAD-65) suggests that they derive from a common ancestral
GAD.
#cross-references MUID:94375018
#contents annotation: intron-exon boundaries
#comment This enzyme (GAD) catalyzes the formation of an inhibitory
neurotransmitter, gamma-aminobutyric acid, from L-glutamic acid;
it has several isoforms, each encoded by a separate gene. GAD has
also been implicated as an autoantigen in autoimmune disease
stiff-man syndrome and insulin-dependent diabetes mellitus.
GENETICS
#gene GDB:GAD2
##cross-references GDB:128595; OMIM:138275
#map_position 10p11.23-10p11.23
CLASSIFICATION
#superfamily human glutamate decarboxylase
KEYWORDS
carbon-carbon lyase; carboxy-lyase; phosphoprotein; pyridoxal
phosphate
FEATURE
396 #binding_site pyridoxal phosphate (lys) (covalent)
#status predicted
SUMMARY
#length 585 #molecular_weight 65411 #checksum 4799
Query Match 100.0%; Score 154; DB 1; Length 585;
Best Local Similarity 100.0%; Pred. No. 5,28e-19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 146 NWELADOPONLEILHCOT 165
|||||
OY 1 NWELADOPONLEILHCOT 20
|||||

Kaufman, D.L.; Wagner-McPherson, C.B.; Evans, G.A.; Tobin,
A.J.
#journal Proc. Natl. Acad. Sci. U.S.A. (1992) 89:2115-2119
#title Two human glutamate decarboxylases, 65-kDa GAD and 67-kDa
#cross-references MUID:92196068
#accession A41935
##molecule_type mRNA
##residues 1-585 ##label BU1
##cross-references GB:M81882; NID:g182933; PIDN:AAA62367.1; PID:g182934
##experimental_source brain
#note sequence extracted from NCBI backbone (NCBIP:88007)
REFERENCE
#authors Karlsten, A.E.; Hagopian, W.A.; Grubin, C.E.; Dube, S.;
Disteche, C.M.; Adler, D.A.; Baetmeier, H.; Mathewes, S.;
Grant, F.J.; Foster, D.; Lermarck, A.
#journal Proc. Natl. Acad. Sci. U.S.A. (1991) 88:8337-8341
#title Cloning and primary structure of a human islet isoform of
glutamic acid decarboxylase from chromosome 10.
#cross-references MUID:92020848
#accession A41292
##molecule_type mRNA
##residues 1-585 ##label KAR
##cross-references GB:M74826; NID:g182931; PIDN:AAA58491.1; PID:g182932
##experimental_source pancreatic islet
REFERENCE
#authors Mauch, L.; Abney, C.C.; Berg, H.; Scherbaum, W.A.; Liedvogel,
B.; Northemann, W.
#journal Eur. J. Biochem. (1993) 212:597-603
#title Characterization of a linear epitope within the human
pancreatic 64-kDa glutamic acid decarboxylase and its
autoimmune recognition by sera from insulin-dependent
diabetes mellitus patients.
#cross-references MUID:93185681
#accession S30058
##molecule_type mRNA
##residues 6-585 ##label MAU
##cross-references EMBL:X69936
##experimental_source pancreatic islet
REFERENCE
#authors Bu, D.F.; Tobin, A.J.
#journal Genomics (1994) 21:222-228
#title The exon-intron organization of the genes (GAD1 and GAD2)
encoding two human glutamate decarboxylases (GAD-67 and
GAD-65) suggests that they derive from a common ancestral
GAD.
#cross-references MUID:94375018
#contents annotation: intron-exon boundaries
#comment This enzyme (GAD) catalyzes the formation of an inhibitory
neurotransmitter, gamma-aminobutyric acid, from L-glutamic acid;
it has several isoforms, each encoded by a separate gene. GAD has
also been implicated as an autoantigen in autoimmune disease
stiff-man syndrome and insulin-dependent diabetes mellitus.
GENETICS
#gene GDB:GAD2
##cross-references GDB:128595; OMIM:138275
#map_position 10p11.23-10p11.23
CLASSIFICATION
#superfamily human glutamate decarboxylase
KEYWORDS
carbon-carbon lyase; carboxy-lyase; phosphoprotein; pyridoxal
phosphate
FEATURE
396 #binding_site pyridoxal phosphate (lys) (covalent)
#status predicted
SUMMARY
#length 585 #molecular_weight 65402 #checksum 7756
Query Match 92.2%; Score 142; DB 1; Length 585;
Best Local Similarity 95.0%; Pred. No. 3,27e-16;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Db 146 NWELADOPONLEILHCOT 165
|||||
OY 1 NWELADOPONLEILHCOT 20
|||||

RESULT 4
ENTRY 538533 #type complete
#journal Lee, D.S.; Tian, J.; Phan, T.; Kaufman, D.L.
#title Biochim. Biophys. Acta (1993) 1216:157-160
#cross-references MUID:94032481
#accession S38533
#status preliminary
##molecule_type mRNA
##residues 1-585 ##label LEE

```

##cross-references GB:LI6980; NID:g413867; PIDN:AAA93049.1; PID:g413868  
COMMENT This enzyme (GAD) catalyzes the formation of an inhibitory  
neurotransmitter, gamma-aminobutyric acid, from L-glutamic acid;  
it has several isoforms, each encoded by a separate gene.  
CLASSIFICATION #superfamily human glutamate decarboxylase  
KEYWORDS carbon-carbon lyase; carboxy-lyase; phosphoprotein; pyridoxal  
phosphate  
FEATURE  
396 #binding-site pyridoxal phosphate (lys) (covalent)  
#status predicted  
SUMMARY #length 585 #molecular-weight 65224 #checksum 7599  
Query Match 92.28; Score 142; DB 1; Length 585;  
Best Local Similarity 92.08; Pred. No. 3,27e-16;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Db 146 NMEADQPONLEETLHCQT 165  
|||||  
QY 1 NMEADQPONLEETLHCQT 20  
RESULT 5  
ENTRY 159173 #type complete  
TITLE glutamate decarboxylase - rat  
ALTERNATE\_NAMES #formal\_name Rattus norvegicus #common\_name Norway rat  
ORGANISM 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change  
DATE 22-Jun-1999  
ACCESSIONS 159173  
REFERENCE 159173  
#authors Bond, R.W.; Wyborski, R.J.; Gottlieb, D.I.  
#journal Proc. Natl. Acad. Sci. U.S.A. (1990) 87:8771-8775  
#title Developmentally regulated expression of an exon containing a  
stop codon in the gene for glutamic acid decarboxylase.  
#cross-references MIMD:91062362  
#accession I59173  
##status preliminary; translated from GB/EMBL/DBJ  
##molecule\_type mRNA  
##residues 1-223 ##label RES  
##cross-references GB:M8350; NID:g204231; PIDN:AAA41185.1; PID:g204232  
CLASSIFICATION #superfamily human glutamate decarboxylase  
SUMMARY #length 223 #molecular-weight 25069 #checksum 1388  
Query Match 55.88; Score 86; DB 2; Length 223;  
Best Local Similarity 52.98; Pred. No. 4.02e-04;  
Matches 9; Conservative 7; Mismatches 1; Indels 0; Gaps 0;  
Db 156 ELSDPESLEQILVDCR 172  
|||  
QY 3 ELADQPONLEETLHCQ 19  
RESULT 6  
ENTRY S61534 #type complete  
TITLE glutamate decarboxylase (EC 4.1.1.15) 62K isoform - mouse  
ALTERNATE\_NAMES glutamic acid decarboxylase  
ORGANISM #formal\_name Mus musculus #common\_name house mouse  
DATE 19-Mar-1997 #sequence\_revision 25-Apr-1997 #text\_change  
22-Jun-1999  
ACCESSIONS S61534; S61533  
REFERENCE S61534  
#authors Katarova, Z.; Szabo, G.; Mugnai, E.; Greenspan, R.J.  
#journal Eur. J. Neurosci. (1990) 2:190-202  
#title Molecular identification of the 62 kd form of glutamic acid  
decarboxylase from the mouse.  
#accession S61534  
##molecule\_type mRNA  
##residues 1-585 ##label KAT  
##cross-references EMBL:249976  
#experimental\_source brain  
REFERENCE S61533  
#authors Szabo, G.  
#submission submitted to the EMBL Data Library, June 1995  
#accession S61533

##molecule\_type mRNA  
##residues 1-534, 'YQPGDKNFRWYISNPASQSDIDTEETIERLQDL' ##label  
SZA  
##cross-references EMBL:249976; NID:9886686; PIDN:CAA90277.1;  
PID:9886687  
#experimental\_source brain  
#note the differences at the carboxyl end are due to a  
frameshift error  
CLASSIFICATION #superfamily human glutamate decarboxylase  
KEYWORDS carbon-carbon lyase; carboxy-lyase  
SUMMARY #length 585 #molecular-weight 65381 #checksum 5716  
Query Match 55.88; Score 86; DB 2; Length 585;  
Best Local Similarity 52.98; Pred. No. 4.02e-04;  
Matches 9; Conservative 7; Mismatches 1; Indels 0; Gaps 0;  
Db 156 ELSDPESLEQILVDCR 172  
|||  
QY 3 ELADQPONLEETLHCQ 19  
RESULT 7  
ENTRY A41367 #type complete  
TITLE glutamate decarboxylase (EC 4.1.1.15) 1 - rat  
ALTERNATE\_NAMES glutamate decarboxylase GAD67; L-glutamate 1-carboxy-lyase  
ORGANISM #formal\_name Rattus norvegicus #common\_name Norway rat  
DATE 12-Jun-1992 #sequence\_revision 23-Mar-1995 #text\_change  
18-Jun-1999  
ACCESSIONS A41367; A43756; JH0195  
REFERENCE A41367  
#authors Michelsen, B.K.; Petersen, J.S.; Boel, E.; Moldrup, A.;  
Dyrberg, T.; Madsen, O.D.  
#journal Proc. Natl. Acad. Sci. U.S.A. (1991) 88:8754-8758  
#title Cloning, characterization, and autoimmune recognition of rat  
islet glutamic acid decarboxylase in insulin-dependent  
diabetes mellitus.  
#cross-references MIMD:92020930  
#accession A41367  
##status preliminary  
##molecule\_type mRNA  
##residues 1-593 ##label MIC  
##cross-references GB:M76177; NID:g204227; PIDN:AAA41184.1; PID:g204228  
REFERENCE A43756  
#authors Wyborski, R.J.; Bond, R.W.; Gottlieb, D.I.  
#journal Brain Res. Mol. Brain Res. (1990) 8:193-198  
#title Characterization of a cDNA coding for rat glutamic acid  
decarboxylase  
#cross-references MIMD:91014554  
#accession A43756  
##status preliminary  
##molecule\_type mRNA  
##residues 1-593 ##label WYB  
##cross-references GB:X57573; NID:g56183; PIDN:CAA0801.1; PID:g56184  
#note the authors translated the codon TGT for residue 412 as  
Ser and TCT for residue 413 as Cys  
REFERENCE JH0195  
#authors Julien, J.F.; Samama, P.; Mallet, J.  
#journal J. Neurochem. (1990) 54:703-705  
#title Rat brain glutamic acid decarboxylase sequence deduced from a  
cloned cDNA.  
#cross-references MIMD:90132703  
#accession JH0195  
##molecule\_type mRNA  
##residues 1-102, 'V', 104-283, 'S', 285-286, 'AD', 289-343, 'EA', 346, 'I',  
348-351, 'LE', 354-379, 'R', 381-593 ##label UTL  
COMMENT This enzyme (GAD) catalyzes the formation of an inhibitory  
neurotransmitter, gamma-aminobutyric acid, from L-glutamic acid;  
it has several isoforms, each encoded by a separate gene.  
CLASSIFICATION #superfamily human glutamate decarboxylase  
KEYWORDS carbon-carbon lyase; carboxy-lyase; phosphoprotein; pyridoxal  
phosphate  
FEATURE

```

404                                #binding_site pyridoxal phosphate (Lys) (covalent)
SUMMARY                            #status predicted
                                   #length 593 #molecular_weight 66640 #checksum 3971

Query Match                        55.8%; Score 86; DB 1; Length 593;
Best Local Similarity 52.9%; Pred. NO. 4.02e-04;
Matches 9; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

Db    156 ELSDHPESLEQILVDCR 172
      |||::|||::|||::| |
Oy    3 ELADQPQLLEEILMHQC   19

RESULT 8
ENTRY          S48135             #type complete
TITLE         glutamate decarboxylase (EC 4.1.1.15) - human
ORGANISM      #formal_name Homo sapiens #common_name man
DATE          14-Jul-1995 #sequence_revision 10-Nov-1995 #text_change
              07-May-1999
ACCESSIONS     S48135
REFERENCE       S48135
#authors       Kelly, C.D.; Edwards, Y.; Johnstone, A.P.; Harfst, E.;
               Nogradi, A.; Nussey, S.S.; Povey, S.; Carter, N.D.
               Ann. Hum. Genet. (1992) 56:255-265
               Nucleotide sequence and chromosomal assignment of a cDNA
               encoding the large isoform of human glutamate
               decarboxylase.
#cross-references MIMD:93080286
#accession      S48135
##residues     ##molecule_type mRNA
##cros-ref     ##residues 1-593 ##label REL
CLASSIFICATION #cross-references EMBL:Z22750
KEYWORDS        #superfamily human glutamate decarboxylase
                carbon-carbon lyase; carboxy-lyase
SUMMARY         #length 593 #molecular-weight 66952 #checksum 4836

Query Match                    55.8%; Score 86; DB 2; Length 593;
Best Local Similarity 52.9%; Pred. NO. 4.02e-04;
Matches 9; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

Db    156 ELSDHPESLEQILVDCR 172
      |||::|||::|||::| |
Oy    3 ELADQPQLLEEILMHQC   19

RESULT 9
ENTRY          S51776             #type complete
TITLE         glutamate decarboxylase (EC 4.1.1.15) - human
ORGANISM      #formal_name Homo sapiens #common_name man
DATE          15-Jul-1995 #sequence_revision 21-Jul-1995 #text-change
              16-Feb-1997
ACCESSIONS     S51776
REFERENCE       S51776
#authors       Johnstone, A.
               submitted to the EMBL Data Library, May 1993
#submission    accession      S51776
               preliminary
               #status      #molecule_type mRNA
               #residues    1-593 #label JOH
               ##cros-ref   ##cross-references EMBL:Z22750
               #note        this is an unpublished revision to the sequence from
               reference S48135
CLASSIFICATION #superfamily human glutamate decarboxylase
KEYWORDS        carbon-carbon lyase; carboxy-lyase
SUMMARY         #length 593 #molecular-weight 66946 #checksum 4842

Query Match                    55.8%; Score 86; DB 2; Length 593;
Best Local Similarity 52.9%; Pred. NO. 4.02e-04;
Matches 9; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

Db    156 ELSDHPESLEQILVDCR 172
      |||::|||::|||::| |
Oy    3 ELADQPQLLEEILMHQC   19
```

```

RESULT      10
ENTRY
TITLE      B41935      #type complete
ALTERNATE_NAMES      glutamate decarboxylase (EC 4.1.1.15) 1 - human
ORGANISM      glutamate decarboxylase GAD67; L-glutamate 1-carboxy-lyase
DATE      #format_name Homo sapiens #common_name man
11-Dec-1993 #sequence_revision 23-Mar-1995 #text_change
18-Jun-1999
ACCESSIONS      B41935; JH0805; JH0806; A61406; PQ0157; PQ0158; B41367;
A36463; A54778
REFERENCE
#authors      A41935
Bu, D.F.; Eriander, M.G.; Hitz, B.C.; Tillakaratne, N.J.K.;
Kautman, D.L.; Wagner-McPherson, C.B.; Evans, G.A.; Todin,
A.J.
Proc. Natl. Acad. Sci. U.S.A. (1992) 89:2115-2119
Two human glutamate decarboxylases, 65-kDa GAD and 67-kDa
GAD, are each encoded by a single gene.
#cross-references MIM:92196068
#accession      B41935
#molecule_type mRNA
#residues      1-594 ##label BUI
#cross-references GB:M81883; NID:g182935; PIDN:AAA62368.1; PID:g182936
#experimental_source pancreatic islet
#note      sequence extracted from NCBI backbone (NCBIP:88006)
REFERENCE
#authors      JH0805
Kawasati, E.; Morichi, R.; Watanabe, M.; Saich, K.; Charle
Brunicaudi, F.; Watt, P.C.; Yamaguchi, T.; Mullen, Y.;
Azazawa, S.; Miyamoto, T.; Nagataki, S.
Biochem. Biophys. Res. Commun. (1993) 192:1353-1359
Cloning and expression of large isoform of glutamic acid
decarboxylase from human pancreatic islet.
#cross-references MIM:93282845
#accession      JH0805
#molecule_type mRNA
#residues      1-177,'N',19-30,'N',32-67,'K',69-115,'L',117-154,'T',
156-301,'C',303-476,'G',478-491,'G',493-594 ##label
KAW
#cross-references GB:S61899; NID:g385310; PIDN:AAB2638.1; PID:g385311
#experimental_source pancreatic islet
REFERENCE
#authors      JH0806
Yamashita, K.; Gram, D.S.; Harrison, L.C.
Biochem. Biophys. Res. Commun. (1993) 192:1347-1352
Molecular cloning of full-length glutamic acid decarboxylase
67 from human pancreas and islets.
#cross-references MIM:93282844
#accession      JH0806
#molecule_type mRNA
#residues      1-67,'K',69-435,'L',437-511,'S',513-594 ##label YAM
#cross-references GB:S61897; NID:g385450; PIDN:AAB2637.1; PID:g385451
#experimental_source pancreatic islet
REFERENCE
#authors      A61406
Kelly, C.; Carter, N.D.; Johnstone, A.P.; Nussey, S.S.
Lancet (1991) 338:1468-1469
Cloning of large isoform of human brain glutamic acid
decarboxylase.
#cross-references MIM:9205769
#accession      A61406
#molecule_type mRNA
#residues      62-67,'K',69-205,'N',207-564,'L',566-594 ##label KEL
#experimental_source brain
REFERENCE
#authors      PQ0157
Gram, D.S.; Barnett, L.D.; Joseph, J.L.; Harrison, L.C.
Biochem. Biophys. Res. Commun. (1991) 176:1239-1244
Cloning and partial nucleotide sequence of human glutamic
acid decarboxylase cDNA from brain and pancreatic islets.
#cross-references MIM:91248209
#accession      PQ0157
#molecule_type mRNA
#residues      218-463 ##label CR1
#cross-references GB:M70438
#experimental_source brain
#accession      PQ0158

```

```

##molecule_type mRNA
##residues 218-234,'K',235-240,'N',242-288,'H',290-323,'L',325-329,'D',331-338,'L',340-380,'S',392-397,##label CR2
##cross-references GB:M0435; NID:g182941; PID:AAAS2513.1; PID:g182942
##experimental_source pancreatic islet
REFERENCE
#authors Michaelson, B.K.; Petersen, J.S.; Boel, E.; Moldrup, A.; Dyrberg, T.; Madsen, O.D.
#journal Proc. Natl. Acad. Sci. U.S.A. (1991) 88:8754-8758
#title Cloning, characterization, and autoimmune recognition of rat islet glutamic acid decarboxylase in insulin-dependent diabetes mellitus.
#cross-references NID:g2020930
#accession B41367
##molecule_type mRNA
##residues 317-482,'R',484-594,##label MITC
REFERENCE
#authors Persson, H.; Peltto-Hulkko, M.; Metsis, M.; Soeder, O.; Brene, S.; Skog, S.; Hoekfelt, T.; Ritzén, E.M.
#journal Mol. Cell. Biol. (1990) 10:4701-4711
#title Expression of the neurotensin-synthesizing enzyme glutamic acid decarboxylase in male germ cells.
#cross-references NID:g9035986
#accession A36463
##molecule_type mRNA
##residues 527-594,##label PER
##cross-references GB:M5574; NID:g182929; PID:AAAT2938.1; PID:g182930
REFERENCE
#authors Bu, D.F.; Tobin, A.J.
#journal Genomics (1994) 21:222-228
#title The exon-intron organization of the genes (GAD1 and GAD2) encoding two human glutamate decarboxylases (GAD-67 and GAD-65) suggests that they derive from a common ancestral
GAD.
#cross-references NID:g94375018
#contents annotation: intron-exon organization
COMMENT This enzyme (GAD) catalyzes the formation of an inhibitory neurotransmitter, gamma-aminobutyric acid, from L-glutamic acid; it has several isoforms, each encoded by a separate gene. GAD has also been implicated as an autoantigen in autoimmune disease stiff-man syndrome and insulin-dependent diabetes mellitus.
GENETICS
#gene GDB:GAD1; GAD
#map_position 2q31-2q31
##cross-references GDB:119244; OMIM:266100
CLASSIFICATION
#superfamily human glutamate decarboxylase
KEYWORDS alternative splicing; carbon-carbon lyase; carboxy-lyase; phosphoprotein; pyridoxal phosphate
FEATURE
405 #binding_site pyridoxal phosphate (Lys) (covalent)
#status predicted
#length 594 #molecular_weight 66924 #checksum 6189
SUMMARY
Query Match 55.8%; Score 86; DB 1; Length 594;
Best Local Similarity 52.9%; Pident.No.4.02e-04;
Matches 9; Conservative 7; Mismatches 1; Indels 0; Gaps 0;
Db 157 ELSDPESLEQLVDCR 173
II:II:II:II:II:II:II:
QY 3 ELADQPNLEFIIMHCQ 19
RESULT 11
ENTRY JCA065 #type complete
TITLE glutamate decarboxylase (EC 4.1.1.15) 67k chain - pig
ORGANISM #formal_name Sus scrofa domestica #common_name domestic pig
DATE 30-Jun-1995 #sequence_revision 14-Jul-1995 #text_change 22-Jun-1999
ACCESSIONS JCA065
REFERENCE JCA064
#authors Suzuki, R.; Asami, N.; Amann, E.; Wagatsuma, M.
#journal Gene (1995) 152:257-260
#title Sequences of two porcine glutamic acid decarboxylases (65-and

```

```

67-kDa GAD)
#cross-references MUID:95137399
#accession JC4065
##molecule-type mRNA
##residues 1-594 ##label SUZ
##cross-references DBRef:D31849; NID:g790966; PIDN:BAA0636.1;
PID:d1007208; PID:g799967

COMMENT ##experimental_source brain
This enzyme catalyzes the conversion of glutamic acid into gamma-amino butyric acid.

CLASSIFICATION #superfamily human glutamate decarboxylase
KEYWORDS carbon-carbon lyase; carboxy-lyase
FEATURE
402-405 #domain DOPA decarboxylase binding #status predicted
SUMMARY #length 594 #molecular-weight 66894 #checksum 5491

Query Match 55.8%; Score 86; DB 2; Length 594;
Best Local Similarity 52.9%; Pred. NO. 4.02e-04;
Matches 9; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

Db 157 ELSDPESLEQILVDCR 173
|||:::||::|:
OY 3 ELAQPNLEIIMHCQ 19

RESULT 12
ENTRY S51775 #type complete
TITLE glutamate decarboxylase (EC 4.1.1.15) - human
ORGANISM #formal_name Homo sapiens; #common name man
DATE 15-Jul-1995 #sequence_revision 21-Jul-1995 #text_change
22-Jun-1999

ACCESSIONS S51775
REFERENCE S51775
#authors Johnstone, A.
#submission submitted to the EMBL Data Library, May 1993
#accession S51775
##status preliminary
##molecule_type mRNA
##residues 1-594 ##label JOH
##cross-references EMBL:222750; NID:g298098; PIDN:CAB0435.1;
PID:g298099

CLASSIFICATION #superfamily human glutamate decarboxylase
KEYWORDS carbon-carbon lyase; carboxy-lyase
SUMMARY #length 594 #molecular-weight 66973 #checksum 6437

Query Match 55.8%; Score 86; DB 2; Length 594;
Best Local Similarity 52.9%; Pred. NO. 4.02e-04;
Matches 9; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

Db 157 ELSDPESLEQILVDCR 173
|||:::||::|:
OY 3 ELAQPNLEIIMHCQ 19

RESULT 13
ENTRY A46758 #type complete
TITLE glutamate decarboxylase (EC 4.1.1.15) 1 - cat
ALTERNATE_NAMES glutamate decarboxylase GAD67; L-glutamate 1-carboxy-lyase
ORGANISM #formal_name Felis silvestris catus; #common name domestic cat
DATE 31-Dec-1993 #sequence_revision 23-Mar-1995 #text_change
18-Jun-1999

ACCESSIONS A46758; A45671
REFERENCE A46758
#authors Kobayashi, Y.; Kaufman, D.L.; Tobin, A.J.
#submission Submitted to Genbank, September 1989
#accession A46758
##molecule_type mRNA
##residues 1-594 ##label KOB
##cross-references GB:M18856; NID:g163858; PIDN:AAS1430.1; PID:g163859

REFERENCE A45671
#authors Kobayashi, Y.; Kaufman, D.L.; Tobin, A.J.
#journal J. Neurosci. (1987) 7:2768-2772
```

```
#title      Glutamic acid decarboxylase CDNA: nucleotide sequence  
            encoding an enzymatically active fusion protein.  
#cross-references MIMD:87310623  
#accession A43671  
#molecule_type mRNA  
#residues   1-558,'RGTRPTFGSGSSRTQLHSPILTSSSR' #label KO2  
#note       This enzyme (GAD) catalyzes the formation of an inhibitory  
            neurotransmitter, gamma-aminobutyric acid, from L-glutamic acid;  
            it has several isoforms, each encoded by a separate gene.  
  
GENETICS  
#gene        GADI  
CLASSIFICATION #superfamily human glutamate decarboxylase  
KEYWORDS     carbon-carbon lyase; carboxy-lyase; phosphoprotein; pyridoxal  
             phosphate  
  
FEATURE  
A05          #binding-site pyridoxal phosphate (Lys) (covalent)  
             #status predicted  
SUMMARY    #length 594 #molecular-weight 66824 #checksum 5630  
  
Query Match      55.8%; Score 86; DB 1; Length 594;  
Best Local Similarity 52.9%; Pred. No. 4,02e-04;  
Matches         9; Conservative 7; Mismatches 1; Indels 0; Gaps 0;
```

RESULT	14	
ENTRY		
TITLE		
ORGANISM		
DATE		
ACCESSIONS		
REFERENCE		
ENTRY		
TITLE		
ORGANISM		
DATE		
ACCESSIONS		
REFERENCE		
ENTRY		
TITLE		
ORGANISM		
DATE		
ACCESSIONS		
REFERENCE		

```

#authors      Croci, L.; Bossolasco, M.; Consalez, G.G.
#submitter    Submitted to the EMBL Data Library, December 1997
#accession    T14159
#status       preliminary; translated from GB/EMBL/DBD
#molecule_type  mRNA
#residues     1-1216 #label CRO
#cross-references  EMBL:AF040964; NID:g3098417; P1D:g3098418;
                  PIDN:AA15635.1

GENETICS
#note         P140
SUMMARY       #length 1216 #molecular-weight 130768 #checksum 9690

Query Match      42.9%; Score 66; DB 2; Length 1216;
Best Local Similarity 37.5%; Pred. NO. 1.91e+00;
Matches 6; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

DB      834 LKEPQRUDGLKRCR 849
      |::||:::|:::|
Oy      4 LADPQNLEITIMRCQ 19

```

```
Search completed: Tue Mar 7 21:26:06 2000
Job time : 8 secs.
```

\*\*\*\*\*  
 W O R L D  
 (TM)  
 \*\*\*\*\*

Release 3.1a John F. Collins, Biocomputing Research Unit.  
 Copyright (c) 1993-1998 University of Edinburgh, U.K.  
 Distribution rights by Oxford Molecular Ltd

Mparch\_pp protein - protein database search, using Smith-Waterman algorithm  
 Run on: Tue Mar 7 21:23:40 2000; Maspar time 3.50 Seconds  
 170.742 Million cell updates/sec  
 Tabular output not generated.

Title: >US-08-981-824-3  
 Description: (1-20) from US08981824.pep  
 Perfect Score: 154  
 Sequence: 1 NMEIADQPQNLEETIMHCQT 20

Scoring table:  
 PAM 150  
 Gap 15

Searched: 82229 segs, 29864866 residues

Post-processing: Minimum Match 0%  
 Listing first 45 summaries

Database:  
 swissprot38  
 1:swissprot

Statistics  
 Mean -29.965; Variance 40.389; scale 0.742

Pred. No. is the number of results predicted by chance to have a  
 score greater than or equal to the score of the result being printed,  
 and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	154	100.0	585	1	DCE2_PIG	1.14e-21
2	154	100.0	585	1	DCE2_HUMAN	1.14e-21
3	142	92.2	585	1	DCE2_MOUSE	1.53e-18
4	142	92.2	585	1	DCE2_RAT	1.53e-18
5	86	55.8	583	1	DCE1_MOUSE	4.77e-05
6	86	55.8	583	1	DCE1_RAT	4.77e-05
7	86	55.8	583	1	DCE1_PIG	4.77e-05
8	86	55.8	583	1	DCE1_HUMAN	4.77e-05
9	86	55.8	583	1	DCE1_FELCA	4.77e-05
10	82	53.2	368	1	OXDA_PHOTO	3.45e-04
11	73	47.4	625	1	PANNA_HELAS	2.47e-02
12	65	42.2	341	1	OXDD_HUMAN	8.57e-01
13	65	42.2	1356	1	HEP1_PODAN	1.31e+00
14	64	41.6	1836	1	60S_RIBOSOMAL_PROTEIN	1.31e+00
15	64	41.6	503	1	VS16_TRYBB	1.31e+00
16	64	41.6	664	1	VP2_BPPH6	1.31e+00
17	63	40.9	183	1	R172_YEAST	1.99e+00
18	63	40.9	332	1	RADA_METJA	1.99e+00
19	63	40.9	468	1	YG4K_YEAST	1.99e+00
20	63	40.9	510	1	SYK_SYNJ3	1.99e+00
21	63	40.9	560	1	PHAC_PSEOL	1.99e+00
22	62	40.3	547	1	YHBX_ECOLI	3.01e+00
23	62	40.3	2515	1	TUD_DROME	3.01e+00

ID	RESULT	1	STANDARD	PRT	585 AA.
AC	P48321				
DT	01-FEB-1996 (Rel. 33, Created)				
DT	01-FEB-1996 (Rel. 33, Last sequence update)				
DT	01-FEB-1996 (Rel. 33, Last annotation update)				
DE	GLUTAMATE DECARBOXYLASE, 65 KD ISOFORM (EC 4.1.1.15) (GAD-65)				
DE	(65 KD GLUTAMIC ACID DECARBOXYLASE).				
GN	GAD2 OR GAD65.				
OS	Sus scrofa (Pig).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;				
OC	Eutheria; Cetartiodactyla; Suina; Suidae; Sus.				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE-BRAIN;				
RX	MEDLINE; 95137399.				
RA	SUZUKI R., ASAMI N., AMANN E., WAGATSUMA M.;				
RT	"Sequences of two porcine glutamic acid decarboxylases (65- and				
RT	67-Kda GAD)."				
RL	Gene 152:257-260(1995).				
CC	- FUNCTION: CATALYZES THE PRODUCTION OF GABA.				
CC	- CATALYTIC ACTIVITY: L-GLUTAMATE + 4-AMINOBUTANOATE + CO(2).				
CC	- COFACTOR: PYRIDOXAL PHOSPHATE.				
CC	- SUBUNIT: HOMODIMER (BY SIMILARITY).				
CC	- SIMILARITY: BELONGS TO GROUP II DECARBOXYLASES (DDC, GAD, HDC AND TYRDC).				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration				
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation				
CC	at the European Bioinformatics Institute. There are no restrictions on its				
CC	use by non-profit institutions as long as its content is in no way				
CC	modified and this statement is not removed. Usage by and for commercial				
CC	entities requires a license agreement (see <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a>				
CC	or send an email to <a href="mailto:license@sib-sib.ch">license@sib-sib.ch</a> ).				
CC	EMBL; D31848; BAA06635.1; -				
DR	PROSITE; PS00392; DDC_GAD_HDC_YDC; 1.				
DR	PFAM; PF00282; pyridoxal.dec; 1.				
KW	Neurotransmitter biosynthesis; lysase; Decarboxylase;				
KW	Pyridoxal phosphate; Multigene family.				
FT	BINDING 356 356 PYRIDOXAL PHOSPHATE (POTENTIAL).				
SQ	SEQUENCE 585 AA; 65388 MW; F3E9BD88 CRC32;				

## ALIGNMENTS

ALIGNMENTS

Query Match 100.0%; Score 154; DB 1; Length 585;  
 Best Local Similarity 100.0%; Pred. No. 1.14e-21;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 146 NWELADQPONLEILMHCOT 165  
 OY 1 NWELADQPONLEILMHCOT 20

RESULT 2  
 ID DCE2\_HUMAN STANDARD: PRT: 585 AA.  
 AC Q05329;  
 DT 01-FEB-1996 (Rel. 33, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 01-FEB-1996 (Rel. 33, Last annotation update)  
 DE GLUTAMATE DECARBOXYLASE, 65 KD ISOFORM (EC 4.1.1.15) (GAD-65)  
 DE (65 KD GLUTAMIC ACID DECARBOXYLASE).  
 GN GAD2 OR GAD65.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 OC Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE; 92196068.  
 RA BU D.-F., ERLANDER M.G., HITZ B.C., TILAKARATNE N.J., KAUFMAN D.L.,  
 RA WAGNER-MCHERSON C.B., EVANS G.A., TOBIN A.J.;  
 RT "Two human glutamate decarboxylases, 65-kDa GAD and 67-kDa GAD, are  
 RT each encoded by a single gene."  
 RT Proc. Natl. Acad. Sci. U.S.A. 89:2115-2119(1992).  
 RL [2]  
 RN SEQUENCE FROM N.A.  
 RP MEDLINE; 94375018.  
 RA BU D.-F., TOBIN A.J.;  
 RT "The exon-intron organization of the genes (GAD1 and GAD2) encoding  
 RT two human glutamate decarboxylases (GAD67 and GAD65) suggests that  
 RT they derive from a common ancestral GAD."  
 RL Genomics 21:222-228(1994).  
 RL [3]  
 RN SEQUENCE FROM N.A.  
 RP TISSUE-PANCREATIC ISLETS;  
 RX MEDLINE; 92070848.  
 RA KALISER A.E., HAGOPIAN W.A., GRUBIN C.E., DUBE S., DISTECHE C.M.,  
 RA ADLER D.A., BARREITER H., MATHEWS S., GRANT F.J., FOSTER D.,  
 RA LERNMARK A.;  
 RT "Cloning and primary structure of a human islet isoform of glutamic  
 RT acid decarboxylase from chromosome 10."  
 RT Proc. Natl. Acad. Sci. U.S.A. 88:8337-8341(1991).  
 RL [4]  
 RN SEQUENCE OF 6-585 FROM N.A.  
 RP TISSUE-PANCREAS;  
 RX MEDLINE; 93185681.  
 RA MARCHEL L., ABNEY C.C., BERG H., SCHERBAUM W.A., LIEBVOGEL B.,  
 RA NORTHEMANN W.;  
 RT "Characterization of a linear epitope within the human pancreatic  
 RT 64-kDa glutamic acid decarboxylase and its autoimmune recognition by  
 RT sera from insulin-dependent diabetes mellitus patients."  
 RL Eur. J. Biochem. 212:597-603(1993).  
 CC -1- FUNCTION: CATALYZES THE PRODUCTION OF GABA.  
 CC -1- CATALYTIC ACTIVITY: L-GLUTAMATE = 4-AMINOBUTANOATE + CO(2).  
 CC -1- COFACTOR: PYRIDOXAL PHOSPHATE.  
 CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).  
 CC -1- SIMILARITY: LOCAL TO DOPA DECARBOXYLASE, AND TO PLP-TYPE HISTIDINE  
 CC DECARBOXYLASE.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL; M81882; AAA62367.1; -;  
 CC EMBL; M74826; AAA58491.1; -;  
 CC EMBL; X69936; CAA49554.1; ALT\_INIT.  
 CC EMBL; M70435; AAA52513.1; -;  
 CC PIR; A41292; A41292.

DR PIR: P00158; P00158.  
 DR MIR: 138275; -;  
 DR PROSITE; PS00392; DDC\_GAD\_HDC\_YDC; 1.  
 DR PFAM; PF00282; pyridoxal\_dec; 1.  
 KW Neurotransmitter biosynthesis; Lyase; Decarboxylase;  
 KW Pyridoxal phosphate; Multigene family.  
 FT BINDING 396 396 PYRIDOXAL PHOSPHATE (BY SIMILARITY).  
 SQ SEQUENCE 585 AA; 65411 MW; 8AD62B62 CRC32.

Query Match 100.0%; Score 154; DB 1; Length 585;  
 Best Local Similarity 100.0%; Pred. No. 1,14e-21;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 146 NWELADQPONLEILMHCOT 165  
 OY 1 NWELADQPONLEILMHCOT 20

RESULT 3  
 ID DCE2\_MOUSE STANDARD: PRT: 585 AA.  
 AC P48320; Q35519;  
 DT 01-FEB-1996 (Rel. 33, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 15-JUL-1998 (Rel. 36, Last annotation update)  
 DE GLUTAMATE DECARBOXYLASE, 65 KD ISOFORM (EC 4.1.1.15) (GAD-65)  
 DE (65 KD GLUTAMIC ACID DECARBOXYLASE).  
 GN GAD2 OR GAD65.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-C57BL/6; TISSUE-BRAIN;  
 RX MEDLINE; 94032481.  
 RA LEE D.S., TIAN J., PHAN T., KAUFMAN D.L.;  
 RT "Cloning and sequence analysis of a murine cDNA encoding glutamate  
 RT decarboxylase (GAD65)."  
 RL Biochim. Biophys. Acta 1216:157-160(1993).  
 RL [2]  
 RN SEQUENCE FROM N.A.  
 RC STRAIN-C57BL/6; TISSUE-BRAIN;  
 RX MEDLINE; 97115675.  
 RA ASADA H., KAWAMURA Y., MARYAMA K., KUME H., DING R.G., JI F.Y.,  
 RA KANBARA N., KUZUME H., SANBO M., YAOI T., OBATA K.;  
 RT "Mice lacking the 65 kDa isoform of glutamic acid decarboxylase  
 RT (GAD65) maintain normal levels of GAD67 and GABA in their brains but  
 RT are susceptible to seizures."  
 RL Biochem. Biophys. Res. Commun. 229:891-895(1996).  
 RN [3]  
 RP SEQUENCE OF 175-379 FROM N.A.  
 RC TISSUE-BRAIN;  
 RX MEDLINE; 94062679.  
 RA FAULKNER-JONES B.E., GRAM D.S., KUN J., HARRISON L.C.;  
 RT "Localization and quantitation of expression of glutamate  
 RT decarboxylase genes in pancreatic beta-cells and other peripheral  
 RT tissues of mouse and rat."  
 RL Endocrinology 133:2962-2972(1993).  
 CC -1- FUNCTION: CATALYZES THE PRODUCTION OF GABA.  
 CC -1- CATALYTIC ACTIVITY: L-GLUTAMATE = 4-AMINOBUTANOATE + CO(2).  
 CC -1- COFACTOR: PYRIDOXAL PHOSPHATE.  
 CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).  
 CC -1- SIMILARITY: LOCAL TO DOPA DECARBOXYLASE, AND TO PLP-TYPE HISTIDINE  
 CC DECARBOXYLASE.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL; L16980; AAA93049.1; -;



```

DR EMBL: D42051: BAA22893.1: -.
DR EMBL: S67454: CAB32806.1: -.
DR MGD: MGI:95634: GAD2.
DR PROSITE: PS00392: DDC_GAD_HDC_YDC: 1.
DR PFM: PF00282: Pyridoxal_dec: 1.
KW Neurotransmitter biosynthesis; Lyase; Decarboxylase;
KW Pyridoxal phosphate; Multigene family.
FT BINDING 396 396 PYRIDOXAL PHOSPHATE (POTENTIAL).
FT CONFLICT 259 259 F -> S (IN REF. 2).
FT CONFLICT 319 319 I -> S (IN REF. 3).
FT CONFLICT 325 325 K -> E (IN REF. 2).
FT CONFLICT 499 499 P -> S (IN REF. 2).
SQ SEQUENCE 585 AA: 65224 MW: 9855088 CRC32:

Query Match 92.2%; Score 142; DB 1; Length 585;
Best Local Similarity 95.0%; Pred. No. 1.53e-18;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 146 NWEIADOPONLEILTHCOT 165
OY 1 NWEIADOPONLEILTHCOT 20

RESULT 4
ID DCE2 RAT STANDARD: PRT: 585 AA.
AC Q05683:
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE GLUTAMATE DECARBOXYLASE, 65 KD ISOFORM (EC 4.1.1.15) (GAD-65)
DE (65 KD GLUTAMIC ACID DECARBOXYLASE).
OS GAD2 OR GAD65.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-HIPPOCAMPUS;
RA MEDLINE: 91299343.
RA ERLANDER M.G., TILAKARATNE N.J., FELDBLUM S., PATEL N.,
RA TOBIN A.J.:
RT "Two genes encode distinct glutamate decarboxylases.";
RL Neuron 7:91-100(1991).
CC -1- FUNCTION: CATALYZES THE PRODUCTION OF GABA.
CC -1- CATALYTIC ACTIVITY: L-GLUTAMATE -> 4-AMINOBUTANOATE + CO(2).
CC -1- COFACTOR: PYRIDOXAL PHOSPHATE.
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SIMILARITY: LOCAL TO DOPA DECARBOXYLASE, AND TO PLP-TYPE HISTIDINE
CC DECARBOXYLASE.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: M72422: AAA63488.1: -.
DR PROSITE: PS00392: DDC_GAD_HDC_YDC: 1.
DR PFM: PF00282: Pyridoxal_dec: 1.
KW Neurotransmitter biosynthesis; Lyase; Decarboxylase;
KW Pyridoxal phosphate; Multigene family.
FT BINDING 396 396 PYRIDOXAL PHOSPHATE (POTENTIAL).
SQ SEQUENCE 585 AA: 65402 MW: E35D601A CRC32:

Query Match 92.2%; Score 142; DB 1; Length 585;
Best Local Similarity 95.0%; Pred. No. 1.53e-18;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 146 NWEIADOPONLEILTHCOT 165
OY 1 NWEIADOPONLEILTHCOT 20

```

```

RESULT 5
ID DCE1 MOUSE STANDARD: PRT: 593 AA.
AC P48318:
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE GLUTAMATE DECARBOXYLASE, 67 KD ISOFORM (EC 4.1.1.15) (GAD-67)
DE (67 KD GLUTAMIC ACID DECARBOXYLASE).
OS GAD1 OR GAD67.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RA KATAROVA Z., SZABO G., MUGNAINI E., GREENSPAN R.;
RA "Molecular identification of the 62 kd form of glutamic acid
RT decarboxylase from the mouse.";
RL Eur. J. Neurosci. 2:190-202(1990).
RN [2]
RP SEQUENCE OF 198-403 FROM N.A.
RC TISSUE-BRAIN;
RA MEDLINE: 94062679.
RA FAULKNER-JONES B.E., CRAM D.S., KUN J., HARRISON L.C.:
RT "Localization and quantitation of expression of two glutamate
RT decarboxylase genes in pancreatic beta-cells and other peripheral
RT tissues of mouse and rat.";
RL Endocrinology 133:2962-2972(1993).
CC -1- FUNCTION: CATALYZES THE PRODUCTION OF GABA.
CC -1- CATALYTIC ACTIVITY: L-GLUTAMATE -> 4-AMINOBUTANOATE + CO(2).
CC -1- COFACTOR: PYRIDOXAL PHOSPHATE.
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO GROUP II DECARBOXYLASES (DDC, GAD, HDC AND
CC TYRDC).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: Z49976: CAA90277.1: -.
DR EMBL: S67453: CAB32805.1: -.
DR MGD: MGI:95632: GAD1.
DR PROSITE: PS00392: DDC_GAD_HDC_YDC: 1.
DR PFM: PF00282: Pyridoxal_dec: 1.
KW Neurotransmitter biosynthesis; Lyase; Decarboxylase;
KW Pyridoxal phosphate; Multigene family.
FT BINDING 404 404 PYRIDOXAL PHOSPHATE (POTENTIAL).
FT CONFLICT 234 234 E -> K (IN REF. 2).
FT CONFLICT 258 258 S -> T (IN REF. 1).
FT CONFLICT 360 360 D -> S (IN REF. 1).
SQ SEQUENCE 593 AA: 66584 MW: 63BC57AA CRC32:

Query Match 55.8%; Score 86; DB 1; Length 593;
Best Local Similarity 52.9%; Pred. No. 4.77e-05;
Matches 9; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

Db 156 ELSDHPSLEQIIVDCR 172
OY 3 ELADOPONLEILTHCOT 19

RESULT 6
ID DCE1 RAT STANDARD: PRT: 593 AA.
AC P18088:
DT 01-NOV-1980 (Rel. 16, Created)
DT 01-NOV-1980 (Rel. 16, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)

```







```
FT CARBOHYD 134 134 POTENTIAL.
FT CARBOHYD 196 196 POTENTIAL.
FT CARBOHYD 303 303 POTENTIAL.
FT CARBOHYD 349 349 POTENTIAL.
FT CARBOHYD 365 365 POTENTIAL.
FT CARBOHYD 372 372 POTENTIAL.
FT CARBOHYD 473 473 POTENTIAL.
SQ SEQUENCE 625 AA: 71350 MW: 8D25C3F3 CRC32:

Query Match
Best Local Similarity 47.4%; Score 73; DB 1; Length 625;
Matches 7; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Db 175 SHNEDMLMHC 186
QY 8 PONTLEELMHQ 19

RESULT 12
ID OXDP_HUMAN STANDARD: PRT; 341 AA.
AC Q99489;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-DEC-1999 (Rel. 39, Last annotation update)
DE D-ASPARTATE OXIDASE (EC 1.4.3.1) (DASOX) (DDO).
GN DDO.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RX MEDLINE: 97306065.
RA SETOYAMA C., MURA R.;
RT "Structural and functional characterization of the human brain D-
RT aspartate oxidase."
RT J. Biochem. 121:798-803(1997).
CC -1- FUNCTION: SELECTIVELY CATALYZES THE OXIDATIVE DEMINATION OF D-
CC ASPARTATE AND ITS N-METHYLATED DERIVATIVE, N-METHYL D-ASPARTATE.
CC -1- CATALYTIC ACTIVITY: D-ASPARTATE + H(2)O + O(2) = OXALACETATE +
CC NH(3) + H(2)O(2).
CC -1- COFACTOR: FAD OR 6-HYDROXYFLAVIN ADENINE DINUCLEOTIDE.
CC -1- SUBCELLULAR LOCATION: PEROXISOMAL.
CC -1- ALTERNATIVE PRODUCTS: TWO ISOFORMS, DDO-1 (SHOWN HERE) AND DDO-2;
CC ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -1- SIMILARITY: BELONGS TO THE DAMOX/DASOX FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: D89858; BAA14031.1; -
DR HSSP: P00371; IDAO.
DR MIM: 124450; -
DR PROSITE: PS00677; DAO: 1.
DR PFAM: PF01266; DAO: 1.
KW OXidoreductase; Flavoprotein; FAD; Peroxisome; Alternative splicing.
FT NP_BIND 6 20 FAD (ADP PART) (POTENTIAL).
FT ACT_SITE 223 223 BY SIMILARITY.
FT ACT_SITE 302 302 BY SIMILARITY.
FT SITE 339 341 MICROBODY TARGETING SIGNAL (POTENTIAL).
FT VARSPLIC 95 153 MISSING (IN ISOFORM DDO-2).
SQ SEQUENCE 341 AA: 37535 MW: 0948D6AB CRC32:

Query Match
Best Local Similarity 42.2%; Score 65; DB 1; Length 341;
Matches 7; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

Db 241 DWNLSFDAENSRRLSNC 258
```

```
QY 1 NWELADDPONTLEELMHC 18

RESULT 13
ID HETL_PODAN STANDARD: PRT; 1356 AA.
AC Q00808;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE VEGETABLE INCOMPATIBILITY PROTEIN HET-E-1.
GN HET-E1.
OS Podospora anserina.
OC Eukaryota; Fungi; Ascomycota; Euascomycetes; Pyrenomycetes;
OC Sordariales; Sordariaceae; Podospora.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 96009891.
RA SAUPE S., TURCO B., BEGUERET J.;
RT "A gene responsible for vegetative incompatibility in the fungus
RT Podospora anserina encodes a protein with a GTP-binding motif and G
RT beta homologous domain."
RT Gene 162:135-139(1995).
CC -1- FUNCTION: RESPONSIBLE FOR VEGETATIVE INCOMPATIBILITY THROUGH
CC SPECIFIC INTERACTIONS WITH DIFFERENT ALLELES OF THE UNLINKED GENE,
CC HET-C.
CC -1- SIMILARITY: CONTAINS 10 WD REPEATS (TRP-ASP DOMAINS).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: L28125; AAA85775.1; -
DR PROSITE: PS00678; WD_REPEATS; 10.
DR PFAM: PF00400; WD40; 10.
KW GTP-Binding; Repeat; WD repeat.
FT NP_BIND 300 307 GTP (POTENTIAL).
FT REPEAT 839 869 WD1.
FT REPEAT 881 911 WD2.
FT REPEAT 923 953 WD3.
FT REPEAT 965 995 WD4.
FT REPEAT 1007 1037 WD5.
FT REPEAT 1049 1079 WD6.
FT REPEAT 1091 1121 WD7.
FT REPEAT 1133 1163 WD8.
FT REPEAT 1175 1205 WD9.
FT REPEAT 1217 1247 WD10.
SQ SEQUENCE 1356 AA: 149765 MW: 96B8E37B CRC32:

Query Match
Best Local Similarity 42.2%; Score 65; DB 1; Length 1356;
Matches 7; Conservative 8; Mismatches 1; Indels 0; Gaps 0;

Db 585 DVSDDPELEIYKLC 600
QY 3 ELADDPONTLEELMHC 18

RESULT 14
ID R171_YEAST STANDARD: PRT; 183 AA.
AC P05740;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE 60S RIBOSOMAL PROTEIN L17-A (YL17-A).
GN RPL17A OR RPL17 OR YKL180W.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Hemiascomycetes; Saccharomycetales;
OC Saccharomycetaceae; Saccharomyces.
```

```

RN [1]
RP SEQUENCE FROM N.A.
RA WIMMANN S., VOSS H., SCHWAGER C., RUPP T., GROTHUES D., SENSEN C.,
RA ZIMMERMANN J., ZIMMERMANN J., ERFLE H., HEWITT N., ANSGORGE W.;
RL Submitted (MAR-1994) to the EMBL/Genbank/DBJ databases.
RN [2]
RP SEQUENCE OF 1-113 FROM N.A.
RX MEDLINE: 94205264.
RA WIMMANN S., VOSS H., SCHWAGER C., RUPP T., STEGEMANN J.,
RA ZIMMERMANN J., GROTHUES D., SENSEN C., ERFLE H., HEWITT N.,
RA BARREY A., ANSGORGE W.;
RT "Sequencing and analysis of 51.6 kilobases on the left arm of
RT chromosome XI from Saccharomyces cerevisiae reveals 23 open reading
RT frames including the FAS1 gene."
RL Yeast 9:1343-1348(1993).
RN [3]
RP PRELIMINARY SEQUENCE OF 1-40.
RA OTAKA E., HIGO K.-I., ITOH T.;
RT "Yeast ribosomal proteins: VIII. Isolation of two proteins and
RT sequence characterization of twenty-four proteins from cytoplasmic
RT ribosomes."
RL Mol. Gen. Genet. 195:544-546(1984).
CC -1- MISCELLANEOUS: THERE ARE TWO GENES FOR L17 IN YEAST.
CC -1- SIMILARITY: BELONGS TO THE L22P FAMILY OF RIBOSOMAL PROTEINS.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL: Z28180; CA82023.1; -
DR EMBL: Z28179; CA82022.1; -
DR EMBL: X74151; CA52258.1; -
DR PIR: S38012; S38012.
DR HSSP: P48286; 1BXE.
DR SGD: L0001715; RPL17A.
DR PROSITE: PS00464; RIBOSOMAL_L22; 1.
DR PFAM: PF00237; Ribosomal_L22; 1.
KW Ribosomal protein; Multigene family.
FT INIT MET 0
FT CONFLICT 0
FT SEQUENCE 103 113 AKGDATKLYV -> VCOEYTFMSTR (IN REF. 2).
SQ SEQUENCE 183 AA; 20418 MW; C00DA5F7 CRC32;

Query Match 41.6%; Score 64; DB 1; Length 183;
Best Local Similarity 43.8%; Pred. No. 1.31e+00;
Matches 7; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Db 38 WELTRAKRYLEQVLDH 53
||| ||| |||
OY 2 WELADQPQNLIELIMH 17

RESULT 15
ID VS16_TRYBB STANDARD: PRT; 503 AA.
AC P06014;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 01-MAY-1992 (Rel. 22, Last annotation update)
DE VARIANT SURFACE GLYCOPROTEIN ILTAT 1.3 PRECURSOR (VSG).
OS Trypanosoma brucei brucei.
OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
RN [1]
RP SEQUENCE FROM N.A.
RA RICE-FICHT A.C., CHEN K.K., DONELSON J.E.;
RT "Sequence homologies near the C-termini of the variable surface
RT glycoproteins of Trypanosoma brucei."
RL Nature 294:53-57(1981).
CC -1- FUNCTION: VSG FORMS A COAT ON THE SURFACE OF THE PARASITE. THE
CC TYRANOSOME EVADES THE IMMUNE RESPONSE OF THE HOST BY EXPRESSING
CC A SERIES OF ANTIGENICALLY DISTINCT VSGS FROM AN ESTIMATED 1000

```

```

CC VSG GENES.
CC -1- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR.
CC A SOLUBLE FORM IS RELEASED FROM RUPTURED CELLS BY THE ACTION OF A
CC PI-PLC.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL: J01221; AAA30288.1; -
DR PIR: S09640; S09640.
DR PFAM: PF00913; Trypan_glycop. 1.
KW Glycoprotein; Antigen; Trypanosomiasis; Signal; GPI-anchor; Membrane.
FT SIGNAL 1 29
FT CHAIN 30 480
FT PROPEP 481 503 VARIANT SURFACE GLYCOPROTEIN ILTAT 1.3.
FT DISULFID 42 168 HYDROPHOBIC, REMOVED DURING MATURATION.
FT CARBOHYD 150 206 BY SIMILARITY.
FT CARBOHYD 419 419 POTENTIAL.
FT CARBOHYD 432 432 POTENTIAL.
FT LIPID 480 480 GPI-ANCHOR.
SQ SEQUENCE 503 AA; 54618 MW; 399B4ECE CRC32;

Query Match 41.6%; Score 64; DB 1; Length 503;
Best Local Similarity 41.2%; Pred. No. 1.31e+00;
Matches 7; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Db 304 NWKPADKPMNDYLIKQ 320
||| ||| |||
OY 1 NWELADQPQNLIELIMH 17

Search completed: Tue Mar 7 21:23:47 2000
Job time : 7 secs.

```



```

CC      RL submitted (APR-1997) to the EMBL/GenBank/DDJ databases.
CC      -I- COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).
CC      -I- SIMILARITY: BELONGS TO GROUP II DECARBOXYLASES (DDC, GAD, HDC AND TYRDC).
DR      DR EMBL; Y12257; CAA72934.1; -.
DR      PROSITE; PS00832; DDC_GAD_HDC_YDC; 1.
DR      PFM; PF00283; Pyridoxal_dec; 1.
KW      Lysase: Decarboxylase: Pyridoxal phosphate.
SQ      SEQUENCE 593 AA; 66648 MW; BAFE2E0 CRC32;

Query Match          55.8%; Score 86; DB 11; Length 593;
Best Local Similarity 52.9%; Pred. No. 3,82e-05;
Matches 9; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

Db 156 ELSDNPESLEQIVLCR 172
QY 3 ELADQPQLTEELHMCQ 19
||:|::|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:~

RESULT 3 PRELIMINARY; PRT; 590 AA.
ID QGY158
AC QGY158;
DT 01-MAY-1999 (TREMBREL; 10, Created)
DT 01-MAY-1999 (TREMBREL; 10, Last sequence update)
DT 01-NOV-1999 (TREMBREL; 12, Last annotation update)
DE GLUTAMATE DECARBOXYLASE 67.
GN GAD67.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;
NC Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
[1]
RP SEQUENCE FROM N.A.
RC STRAIN-WHITE LEGHORN;
RW WABERG F.;
RT "Characterization of glutamate decarboxylase in chicken.";
RL Submitted (OCT-1997) to the EMBL/GenBank/DDJ databases.
CC -I- COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).
CC -I- SIMILARITY: BELONGS TO GROUP II DECARBOXYLASES (DDC, GAD, HDC AND TYRDC).
DR EMBL; AF030355; AAD01902.1; -.
DR PROSITE; PS00392; DDC_GAD_HDC_YDC; 1.
KW Lysase: Decarboxylase: Pyridoxal phosphate.
SQ SEQUENCE 590 AA; 66710 MW; 80B6DDF CRC32;

Query Match          53.2%; Score 82; DB 13; Length 590;
Best Local Similarity 52.9%; Pred. No. 2,97e-04;
Matches 9; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

Db 153 ELSDNPESLEQIVLCR 169
QY 3 ELADQPQLTEELHMCQ 19
||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:~

RESULT 4 PRELIMINARY; PRT; 547 AA.
ID Q46994
AC Q46994;
DT 01-NOV-1996 (TREMBREL; 01, Created)
DT 01-NOV-1996 (TREMBREL; 01, Last sequence update)
DT 01-AUG-1998 (TREMBREL; 07, Last annotation update)
DE OUTER MEMBRANE ADHERENCE PROTEIN-ASSOCIATED PROTEIN.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
CN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-O157:H7;
RA ZHAO S., MITCHELL S.E., MENG J., DOYLE M.P., KRESOVICH S.;
RL Submitted (MAR-1996) to the EMBL/GenBank/DDJ databases.
DR EMBL; U50906; AAA96312.1; -.
SQ SEQUENCE 547 AA; 61446 MW; B737EA82 CRC32;

Query Match          42.9%; Score 66; DB 2; Length 547;
Best Local Similarity 53.8%; Pred. No. 6,46e-01;
```

```

Db      497  PEOPOTLEEVH 509
Oy      5  ADOPONLEETIM 17

RESULT  5
ID      070298
AC      070298;
DT      01-AUG-1998 (TREMBLrel. 07, Created)
DT      01-AUG-1998 (TREMBLrel. 07, Last sequence update)
DT      01-AUG-1998 (TREMBLrel. 07, Last annotation update)
DE      P140.
GN      P140.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC      Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN      [1]
RP      SEQUENCE FROM N.A.
RA      CROCI L., BOSSOLASCO M., CONSALFZ G.G.;
RL      Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
DR      EMBL; AF040944; AAC15635.1;
SQ      SEQUENCE 1216 AA; 130768 MW; FB545D0C CRC32;

Query Match      42.9%; Score 66; DB 11; Length 1216;
Best Local Similarity 37.5%; Pred. No. 6,46e-01;
Matches 6; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

Db      834  LKEEPRDGLKRCR 849
Oy      4  LADOPONLEETIMCQ 19

RESULT  6
ID      002356
AC      002356;
DT      01-JUL-1997 (TREMBLrel. 04, Created)
DT      01-JUL-1997 (TREMBLrel. 04, Last sequence update)
DT      01-NOV-1999 (TREMBLrel. 12, Last annotation update)
DE      F35E12.3 PROTEIN.
DE      F35E12.3.
GN      Caenorhabditis elegans.
OS      Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditidae;
OC      Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditidae;
OC      Rhabditina; Rhabditioidea; Rhabditidae; Pelodierinae; Caenorhabditis.
RN      [1]
RP      SEQUENCE FROM N.A.
RA      STEWARD C.;
RL      Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
RN      [2]
RP      SEQUENCE FROM N.A.
RX      MEDLINE; 94150718.
RA      WILSON R., AINSOUDGH R., ANDERSON K., BAYNES C., BEKES M.,
RA      BONEFIELD J., BURTON J., CONNELL M., CORSEY T., COOPER J., COULSON A.,
RA      CRAWTON M., DEAR S., DU Z., DUREIN R., FAVELLO A., FULTON L.,
RA      GARDNER A., GREEN P., HAWKINS T., HILLER L., JIER M., JOHNSTON L.,
RA      JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
RA      LIGHTING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
RA      PARSONS J., PERCY C., RIKKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
RA      SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
RA      THIERYT-WIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
RA      WATSON A., WEINSTOCK L., WILKINSON-SPRAT J., WOHLIDAN P.;
RT      "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT      elegans.";
RL      Nature 368:32-38(1994).
DR      EMBL; Z81527; CAB04271.1;
SQ      SEQUENCE 296 AA; 34465 MW; ED503FA9 CRC32;

Query Match      41.6%; Score 64; DB 5; Length 296;
Best Local Similarity 35.3%; Pred. No. 1.57e+00;
Matches 6; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

235  RDVIDNSNMIESVLIQC 251

```



QY 2 WELADOPONLEILMHC 18

RESULT 7 PRELIMINARY: PRT: 515 AA.  
ID 052215  
AC 052215  
DT 01-JUN-1998 (TReMBLrel. 06, Created)  
DT 01-JUN-1998 (TReMBLrel. 06, Last sequence update)  
DT 01-AUG-1998 (TReMBLrel. 07, Last annotation update)  
DE TRANSPOSASE.  
OS Pseudomonas pseudocataligenes.  
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonas group;  
OC Pseudomonas.  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-JS45;  
RA DAVIS J.K., SOMERVILLE C.C., SPAIN J.C.;  
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF028594; AAB94124.1;  
SQ SEQUENCE 515 AA; 56566 MW; 1BAE619 CRC32;

Query Match 41.6%; Score 64; DB 2; Length 515;  
Best Local Similarity 38.5%; Pred. No. 1.57e+00;  
Matches 5; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

Db 499 DWDLAQPEVDQ 511  
QY 1 NWELADOPONLEE 13

RESULT 8 PRELIMINARY: PRT: 547 AA.  
ID P74269  
AC P74269  
DT 01-FEB-1997 (TReMBLrel. 02, Created)  
DT 01-FEB-1997 (TReMBLrel. 02, Last sequence update)  
DT 01-JAN-1999 (TReMBLrel. 09, Last annotation update)  
DE ALPHA-ISOPROPYLALATE SYNTHASE.  
GN LEUA.  
OS Synecocystis sp. (strain PCC 6803).  
OC Bacteria; Cyanobacteria; Chroococcales; Synecocystis.  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-PCC6803;  
RA TABATA S.;  
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN-PCC6803;  
RX MEDLINE; 97061201.  
RA KANEKO T., SATO S., KOTANI H., TANAKA A., ASAMIZU E., NAKAMURA Y.,  
RA MIYAJIMA N., HIROSAWA M., SUGIURA M., SASAMOTO S., KIMURA T.,  
RA HOSOGUCHI T., MATSUNO A., MURAKI A., NAKAZAKI N., NARIO K., OKUMURA S.,  
RA SHIMPO S., TAKEUCHI C., WADA T., WATANABE A., YAMADA M.,  
RA TABATA S.;  
RT "Sequence analysis of the genome of the unicellular cyanobacterium  
RT Synecocystis sp. strain PCC6803. II. Sequence determination of the  
RT entire genome and assignment of potential protein-coding regions.";  
RL DNA Res. 3:109-136(1996).  
DR EMBL; D90913; BAA18363.1;  
DR PFAM; PF00882; HMG-Like; 1.  
SQ SEQUENCE 547 AA; 59819 MW; 6FDA2E7C CRC32;

Query Match 41.6%; Score 64; DB 2; Length 547;  
Best Local Similarity 36.8%; Pred. No. 1.57e+00;  
Matches 7; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

Db 62 WOLOEPLEQAEIVAFCS 80  
QY 2 WELADOPONLEILMHCOT 20

RESULT 9

ID 026912 PRELIMINARY: PRT: 3229 AA.  
AC 026912  
DT 01-NOV-1996 (TReMBLrel. 01, Created)  
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)  
DT 01-NOV-1998 (TReMBLrel. 08, Last annotation update)  
DE PROTEIN 1 OF A DISPERSED GENE FAMILY (DGF-1).  
GN DGF-1.  
OS Trypanosoma cruzi.  
OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE; 93063053.  
RA WINCKER P., MURTA-DOVALES A.C., GOLDBERG S.;  
RT "Nucleotide sequence of a representative member of a Trypanosoma cruzi  
RT dispersed gene family.";  
RL Mol. Biochem. Parasitol. 55:217-220(1992).  
DR EMBL; M90534; AAA30182.1;  
SQ SEQUENCE 3229 AA; 334929 MW; F75E94C3 CRC32;

Query Match 41.6%; Score 64; DB 5; Length 3229;  
Best Local Similarity 35.3%; Pred. No. 1.57e+00;  
Matches 6; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

Db 730 WTFNAPQOTLITLHC 746  
QY 2 WELADOPONLEILMHC 18

RESULT 10 PRELIMINARY: PRT: 162 AA.  
ID 09YCX4  
AC 09YCX4  
DT 01-NOV-1999 (TReMBLrel. 12, Created)  
DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)  
DT 01-NOV-1999 (TReMBLrel. 12, Last annotation update)  
DE 162AA LONG HYPOTHETICAL PROTEIN.  
GN APEL138.  
OS Aeropyrum pernix.  
OC Archaea; Crenarchaeota; Aeropyrum.  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-K1;  
RX MEDLINE; 99310339.  
RA KAWARABAYASHI Y., HINO Y., HORIKAWA H., YAMAZAKI S., HAIKAWA Y.,  
RA JIN-NO K., TAKAHASHI M., SEKINE M., BABA S., ANKAI A., KOSUGI H.,  
RA HOSOGUCHI A., FUKUI S., NAGAI Y., NISHIJIMA K., NAKAZAWA H.,  
RA TAKAMURA M., MASUDA S., FUNAHASHI T., TANAKA T., KUOH Y.,  
RA YAMAZAKI J., KUSHIDA N., OGUCHI A., AOKI K., KUBOTA K., NAKAMURA Y.,  
RA NOMURA N., SAKO Y., KIRUCHI H.;  
RT "Complete genome sequence of an aerobic hyper-thermophilic  
RT crenarchaeon, Aeropyrum pernix K1.";  
RL DNA Res. 6:83-101(1999).  
DR EMBL; AP000060; BAA80123.1;  
SQ SEQUENCE 162 AA; 17732 MW; 90001DD CRC32;

Query Match 40.9%; Score 63; DB 1; Length 162;  
Best Local Similarity 43.8%; Pred. No. 2.44e+00;  
Matches 7; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Db 9 WKLEQSESELEIALR 24  
QY 2 WELADOPONLEILMH 17

RESULT 11 PRELIMINARY: PRT: 533 AA.  
ID 09Z435  
AC 09Z435  
DT 01-MAY-1999 (TReMBLrel. 10, Created)  
DT 01-MAY-1999 (TReMBLrel. 10, Last sequence update)  
DT 01-MAY-1999 (TReMBLrel. 10, Last annotation update)  
DE POLY(HYDROXYALKANONATE) SYNTHASE (FRAGMENT).  
GN PHAC2.  
OS Pseudomonas putida.  
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonas group;

OC Pseudomonas.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BMO1;  
 RA VALENTIN H.E., STUART E.S., FULLER R.C., LENZ R.W., DENNIS D.;  
 RT "Investigation of the function of proteins associated to  
 RT polyhydroxyalkanoate) inclusions in Pseudomonas putida BMO1.";  
 RL J. Biotechnol. 0:0-0(1998).  
 DR EMBL: AF042276; AAD02217.1; -.  
 FT NON\_TER  
 SQ SEQUENCE 533 AA; 59894 MW; E038BD80 CRC32;  
 Query Match 40.9%; Score 63; DB 2; Length 533;  
 Best Local Similarity 40.0%; Pred. No. 2.44e+00;  
 Matches 8; Conservative 4; Mismatches 8; Indels 0; Gaps 0;  
 Db 237 EMBL:AF042276; AAD02217.1; -.  
 QY 1 NWELADQPONLEILMHCOT 20

RESULT 12  
 ID 092778 PRELIMINARY; PRT; 652 AA.  
 AC 092778;  
 DT 01-MAY-1999 (TREMBlrel. 10, Created)  
 DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)  
 DE HYPOTHETICAL 72.0 KD PROTEIN.  
 GN F9H3.13.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;  
 OC core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;  
 OC Arabidopsis.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-CV. COLUMBIA.  
 RA HUANG E.N., PARNELL L.D., DE LA BASTIDE M., SCHUTZ K., HABERMANN K.,  
 RA DEDHIA N.N., MCCOMBIE W.R.;  
 RT "Genomic sequence of Arabidopsis thaliana BAC F9H3, chromosome IV,  
 RT 18.8 cm.";  
 RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF071527; AAD11592.1; -.  
 KW Hypothetical protein  
 SQ SEQUENCE 652 AA; 71969 MW; B5B68A6B CRC32;  
 Query Match 40.9%; Score 63; DB 10; Length 652;  
 Best Local Similarity 66.7%; Pred. No. 2.44e+00;  
 Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
 Db 326 HVOLEELILMHC 337  
 QY 7 QPONLEILMHC 18

RESULT 13  
 ID 027929 PRELIMINARY; PRT; 655 AA.  
 AC 027929;  
 DT 01-JAN-1998 (TREMBlrel. 05, Created)  
 DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)  
 DT 01-AUG-1998 (TREMBlrel. 07, Last annotation update)  
 DE CONSERVED PROTEIN.  
 GN MTH1907.  
 OS Methanobacterium thermoautotrophicum.  
 OC Archaea; Euryarchaeota; Methanobacteriales; Methanobacteriaceae;  
 OC Methanobacterium.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-DELTA H.  
 RA MEDLINE: 98037514.  
 RA SMITH D.R., DOCCETTE-STAMM L.A., DELOUGHERY C., LEE H.-M., DUBOIS J.,  
 RA ALDRIDGE T., BASHIRZADEH R., BLAKELY D., COOK R., GILBERT K.,  
 RA HARRISON D., HOANG L., KEAGLE P., LUMM W., POTHIER B., QIU D.,

RA SPADAFORA R., VICARE R., WANG Y., WIERZBOWSKI J., GIBSON R.,  
 RA JIRANI N., CARUSO A., BUSH D., SAFER H., PATMELL D., PRAHAAR S.,  
 RA MCDUGALL S., SHIMER G., GOYAL A., PIETROVSKI S., CHURCH G.M.,  
 RA DANIELS C.J., MAO J.-I., RICE P., NOLLING J., REEVE J.N.;  
 RT "Complete genome sequence of Methanobacterium thermoautotrophicum  
 RT deltaH: functional analysis and comparative genomics.";  
 RL J. Bacteriol. 179:7135-7155(1997).  
 DR EMBL: AE000942; AAB6367.1; -.  
 FT NON\_TER  
 SQ SEQUENCE 655 AA; 75562 MW; 05CC7FD2 CRC32;  
 Query Match 40.9%; Score 63; DB 1; Length 655;  
 Best Local Similarity 50.0%; Pred. No. 2.44e+00;  
 Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;  
 Db 164 LDBHSELEILM 177  
 QY 4 LADQPONLEILM 17

RESULT 14  
 ID 024327 PRELIMINARY; PRT; 1033 AA.  
 AC 024327;  
 DT 01-NOV-1996 (TREMBlrel. 01, Created)  
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
 DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)  
 DE GP160-DTRK PRECURSOR.  
 GN DTRK.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Anthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-CANTON S;  
 RX MEDLINE: 92164624.  
 RA FULIDO D., CAMPUZANO S., KODA T., MODOLELL J., BARBACID M.;  
 RT "Dtrk, a Drosophila gene related to the trk family of neurotrophin  
 RT receptors, encodes a novel class of neural cell adhesion molecule.";  
 RL EMBL: X63453; CAA45053.1; -.  
 DR HSSP: P06213; IIRK.  
 DR FLYBASE: FBgn004839; TK48D.  
 DR PFAM: PF00047; ig: 5  
 DR PFAM: PF00069; pkinase; 1.  
 KW Signal; Cell adhesion.  
 FT SIGNAL  
 FT CHAIN 1  
 SQ SEQUENCE 1033 AA; 114367 MW; 1F8EB944 CRC32;  
 Query Match 40.9%; Score 63; DB 5; Length 1033;  
 Best Local Similarity 42.1%; Pred. No. 2.44e+00;  
 Matches 8; Conservative 6; Mismatches 4; Indels 1; Gaps 1;  
 Db 988 EWSVAETPDSLEILLC 1006  
 QY 1 NWELADQ-PONLEILMHC 18

RESULT 15  
 ID 012175 PRELIMINARY; PRT; 221 AA.  
 AC 012175;  
 DT 01-JUL-1997 (TREMBlrel. 04, Created)  
 DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update)  
 DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)  
 DE ENVELOPE GLYCOPROTEIN (FRAGMENT).  
 GN ENV.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE: 98080455.  
 RA DEWART E.L., MULLINS J.I., GUPTA P., LEARN G.H. JR., HOLODNIT M.,  
 RA KATZENSTEIN D., WALKER B.D., SINGH M.K.;

RT "Human immunodeficiency virus type 1 populations in blood and semen."  
RL J.VIROL.72:617-623(1998).  
DR EMBL: U96510; AAC40359.1; -.  
DR PFAM: PF00516; GP120; 1.  
KW Envelope protein.  
FT NON\_TER 1 1  
FT NON\_TER 221 221  
SQ SEQUENCE 221 AA: 24697 MW: FDB68EB3 CRC32:  
  
Query Match 40.3%; Score 62; DB 14; Length 221;  
Best Local Similarity 27.8%; Pred. No. 3.76e+00;  
Matches 5; Conservative 9; Mismatches 4; Indels 0; Gaps 0;  
  
Db 141 WNTESNNTITLPCR 158  
QY 2 WELADQPNLEILMHCQ 19

Search completed: Tue Mar 7 21:24:16 2000  
Job time : 12 secs.

THIS PAGE BLANK (USE)

(TBM)

DF 55 kD Glutamic acid decarboxylase peptide fragment IV.  
KW GAD, 65 kD; human; glutamic acid decarboxylase; autoreactive; diagnosis;  
KW insulin-dependent diabetes mellitus; IDDM; cell-mediated disease;  
KW predisposition; autoimmune; tumour; rheumatoid arthritis;  
KW multiple sclerosis.  
OS Synthetic.  
PN DE19526561-A1.  
PD 23-JUN-1997.  
PF 20-JUL-1995: 026561.  
PR 20-JUL-1995: DE-026561.  
PI (BOE) -BOEHRINGER/MANNHEIM GMBH.  
PI Donie F, Endl J, Ganz M, Jung G, Kientsch-engel R;  
PI Pozzilli P, Stahl P;  
DR WPI: 97-088254/09.  
PT Skin test for diagnosis of cell-mediated diseases, esp. diabetes -  
PT involving intradermal admin. of auto-reactive substances  
PS Claim 11; Page 9; 12pp; German.  
CC W18842-70 are peptide fragments of the 65 kD human glutamic acid  
CC decarboxylase (GAD). The fragments are autoreactive substances used for  
CC diagnosis of insulin-dependent diabetes mellitus (IDDM). The diagnosis is  
CC determined by using a claimed method for diagnosis of cell-mediated  
CC diseases or a predisposition to cell-mediated diseases, which is effected  
CC by administering an autoreactive substance intradermally and establishing  
CC the diagnosis on the basis of the occurrence or lack of a positive  
CC reaction at the site of administration. The method is used for diagnosis  
CC of autoimmune and tumour diseases, preferably T-cell-mediated diseases  
CC such as rheumatoid arthritis, multiple sclerosis and especially IDDM.  
SQ Sequence 20 AA;

Query Match 100.0%; Score 147; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 3.73e-09;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 TLKXAIKTHPRYNOLSTG 20  
QY 1 TLKXAIKTHPRYNOLSTG 20

RESULT 3  
ID R23645 standard; Protein: 503 AA.  
AC R23645;  
DT 02-NOV-1992 (first entry)  
DE Human GAD65 gene product.  
KW Glutamic acid decarboxylase; IDDM; stiff man syndrome;  
KW autoantibodies.  
OS Homo sapiens.  
PN WO9205446-A.  
PD 02-APR-1992.  
PF 23-SEP-1991: 006872.  
PR 21-SEP-1990: US-586536.  
PA (REGC) UNIV CALIFORNIA.  
PA (REGC) UNIV CALIFORNIA.  
PI Erlanger MG, Kaufman DL, Tobin AJ;  
DR WPI: 92-150489/18.  
DR N-PSDB: 024184.  
PT Novel cDNA encoding GAD65 polypeptide - used to produce GAD65 for  
PT therapeutic and diagnostic application in insulin-dependent  
PT diabetes mellitus patients  
PS Disclosure: Fig 3; 53pp; English.  
CC The sequence given is a glutamic acid decarboxylase (GAD65). GAD65  
CC can be used for the diagnosis and therapy of patients with autoimmune  
CC diseases, esp. insulin-dependant diabetes mellitus (IDDM) and "stiff  
CC man" syndrome. It is possible to use either the entire GAD65 protein  
CC or polypeptide fragments of it for the immunological detection of  
CC autoantibodies to GAD65 which are indicative of IDDM and other auto-  
CC immune diseases. The production of this sequence by recombinant DNA  
CC technology allows large scale production of eukaryotic GAD65 in its  
CC native form without the need for separation from other proteinaceous  
CC prods.  
SQ Sequence 503 AA;

Query Match 100.0%; Score 147; DB 1; Length 503;

Best Local Similarity 100.0%; Pred. No. 3.73e-09;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Db 166 TLKXAIKTHPRYNOLSTG 185  
QY 1 TLKXAIKTHPRYNOLSTG 20

RESULT 4  
ID R59520 standard; protein: 540 AA.  
AC R59520;  
DT 09-NOV-1994 (first entry);  
DE GAD65 1-45 N-terminal-deleted mutant.  
KW GAD65; glutamate-decarboxylase; diabetes mellitus;  
KW stiff man syndrome; autoantibody; mutagenesis.  
OS Homo sapiens.  
PN WO9412529-A.  
PD 09-JUN-1994.  
PF 02-DEC-1993: U11705.  
PR 03-DEC-1992: US-984935.  
PA (REGC) UNIV CALIFORNIA.  
PI Baekkeskov S, Kim J, Narnchuk M, Richter W, Shi Y;  
DR WPI: 94-200193/24.  
PT New soluble fragments of glutamic acid decarboxylase protein -  
PT used for the diagnosis and treatment of insulin dependent  
PT diabetes mellitus and stiff man syndrome.  
PS Disclosure: Fig. 1; 73pp; English.  
CC The amino acid sequences of human GAD65 (R59516) and rat GAD65  
CC (R59517) were determined. New soluble fragments of GAD65  
CC (R59518-25) were prepared by deletion/substitution  
CC mutagenesis. These fragments are free of N-terminal amino acids  
CC that limit solubility. Different fragments contain epitopes for  
CC different classes of GAD65 autoantibodies.  
SQ Sequence 540 AA;

Query Match 100.0%; Score 147; DB 1; Length 540;  
Best Local Similarity 100.0%; Pred. No. 3.73e-09;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 121 TLKXAIKTHPRYNOLSTG 140  
QY 1 TLKXAIKTHPRYNOLSTG 20

RESULT 5  
ID R59521 standard; protein: 540 AA.  
AC R59521;  
DT 09-NOV-1994 (first entry)  
DE GAD65 1-45 N-terminal-deleted mutant.  
KW GAD65; glutamate-decarboxylase; diabetes mellitus;  
KW stiff man syndrome; autoantibody; mutagenesis.  
OS Rattus sp.  
PN WO9412529-A.  
PD 09-JUN-1994.  
PF 02-DEC-1993: U11705.  
PR 03-DEC-1992: US-984935.  
PA (REGC) UNIV CALIFORNIA.  
PI Baekkeskov S, Kim J, Narnchuk M, Richter W, Shi Y;  
DR WPI: 94-200193/24.  
PT New soluble fragments of glutamic acid decarboxylase protein -  
PT used for the diagnosis and treatment of insulin dependent  
PT diabetes mellitus and stiff man syndrome.  
PS Disclosure: Fig. 1; 73pp; English.  
CC The amino acid sequences of human GAD65 (R59516) and rat GAD65  
CC (R59517) were determined. New soluble fragments of GAD65  
CC (R59518-25) were prepared by deletion/substitution  
CC mutagenesis. These fragments are free of N-terminal amino acids  
CC that limit solubility. Different fragments contain epitopes for  
CC different classes of GAD65 autoantibodies.  
SQ Sequence 540 AA;

Query Match 100.0%; Score 147; DB 1; Length 540;  
Best Local Similarity 100.0%; Pred. No. 3.73e-09;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 121 TLKAIKTHPRFYNOLSTG 140

QY 1 TLKAIKTHPRFYNOLSTG 20

RESULT 6  
ID R59525 standard; protein: 544 AA.

AC R59525;

DT 09-NOV-1994 (first entry)

DE GAD65 545-585 C-terminal-deleted mutant.

KW GAD65; glutamate-decarboxylase; diabetes mellitus;

KM stiff man syndrome; autoantibody; mutagenesis.

OS Rattus sp.

PN W09412529-A.

PD 09-JUN-1994.

PF 02-DEC-1993; U11705.

PR 03-DEC-1992; US-984935.

PA (REGC ) UNIV CALIFORNIA.

PI Beekeskov S, Kim J, Namchuk M, Richter W, Shi Y;

DR WPI: 94-200193/24.

PT New soluble fragments of glutamic acid decarboxylase protein -

PT diabetes mellitus and stiff man syndrome.

PS Disclosure; Fig. 1: 73pp; English.

CC The amino acid sequences of human GAD65 (R59516) and rat GAD65

CC (R59517) were determined. New soluble fragments of GAD65

CC (R59518-25) were prepared by deletion/substitution

CC mutagenesis. The C-terminally deleted mutants given in R59524-25

CC are able to recognize IDDM autoantibodies having the specificity

CC of MIC44/MICA6, but not those having the specificity of MIC41/MICA3

CC or MIC42. These mutants also have some N-terminal modifications

CC to improve solubility.

CC Sequence 544 AA;

SQ

Query Match 100.0%; Score 147; DB 1; Length 544;

Best Local Similarity 100.0%; Pred. No. 3.73e-09;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 166 TLKAIKTHPRFYNOLSTG 185

QY 1 TLKAIKTHPRFYNOLSTG 20

RESULT 7  
ID R59524 standard; protein: 544 AA.

AC R59524;

DT 09-NOV-1994 (first entry)

DE GAD65 545-585 C-terminal-deleted mutant.

KW GAD65; glutamate-decarboxylase; diabetes mellitus;

KM stiff man syndrome; autoantibody; mutagenesis.

OS Homo sapiens.

PN W09412529-A.

PD 09-JUN-1994.

PF 02-DEC-1993; U11705.

PR 03-DEC-1992; US-984935.

PA (REGC ) UNIV CALIFORNIA.

PI Beekeskov S, Kim J, Namchuk M, Richter W, Shi Y;

DR WPI: 94-200193/24.

PT New soluble fragments of glutamic acid decarboxylase protein -

PT diabetes mellitus and stiff man syndrome.

PS Disclosure; Fig. 1: 73pp; English.

CC The amino acid sequences of human GAD65 (R59516) and rat GAD65

CC (R59517) were determined. New soluble fragments of GAD65

CC (R59518-25) were prepared by deletion/substitution

CC mutagenesis. The C-terminally deleted mutants given in R59524-25

CC are able to recognize IDDM autoantibodies having the specificity

CC of MIC44/MICA6, but not those having the specificity of MIC41/MICA3

CC or MIC42. These mutants also have some N-terminal modifications

CC to improve solubility.

CC Sequence 544 AA;

SQ

Query Match 100.0%; Score 147; DB 1; Length 544;

Best Local Similarity 100.0%; Pred. No. 3.73e-09;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 166 TLKAIKTHPRFYNOLSTG 185

QY 1 TLKAIKTHPRFYNOLSTG 20

RESULT 8  
ID R59518 standard; protein: 554 AA.

AC R59518;

DT 09-NOV-1994 (first entry)

DE GAD65 1-31 deleted; C45A mutant.

KW GAD65; glutamate-decarboxylase; diabetes mellitus;

KM stiff man syndrome; autoantibody; mutagenesis.

OS Homo sapiens.

PN W09412529-A.

PD 09-JUN-1994.

PF 02-DEC-1993; U11705.

PR 03-DEC-1992; US-984935.

PA (REGC ) UNIV CALIFORNIA.

PI Beekeskov S, Kim J, Namchuk M, Richter W, Shi Y;

DR WPI: 94-200193/24.

PT New soluble fragments of glutamic acid decarboxylase protein -

PT diabetes mellitus and stiff man syndrome.

PS Disclosure; Fig. 1: 73pp; English.

CC The amino acid sequences of human GAD65 (R59516) and rat GAD65

CC (R59517) were determined. New soluble fragments of GAD65

CC (R59518-25) were prepared by deletion/substitution

CC mutagenesis. These fragments are free of N-terminal amino acids

CC that limit solubility. Different fragments contain epitopes for

CC different classes of GAD65 autoantibodies.

CC Sequence 554 AA;

Query Match 100.0%; Score 147; DB 1; Length 554;

Best Local Similarity 100.0%; Pred. No. 3.73e-09;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 135 TLKAIKTHPRFYNOLSTG 154

QY 1 TLKAIKTHPRFYNOLSTG 20

RESULT 9  
ID R59519 standard; protein: 554 AA.

AC R59519;

DT 09-NOV-1994 (first entry)

DE GAD65 1-31 deleted; C45A mutant.

KW GAD65; glutamate-decarboxylase; diabetes mellitus;

KM stiff man syndrome; autoantibody; mutagenesis.

OS Rattus sp.

PN W09412529-A.

PD 09-JUN-1994.

PF 02-DEC-1993; U11705.

PR 03-DEC-1992; US-984935.

PA (REGC ) UNIV CALIFORNIA.

PI Beekeskov S, Kim J, Namchuk M, Richter W, Shi Y;

DR WPI: 94-200193/24.

PT New soluble fragments of glutamic acid decarboxylase protein -

PT diabetes mellitus and stiff man syndrome.

PS Disclosure; Fig. 1: 73pp; English.

CC The amino acid sequences of human GAD65 (R59516) and rat GAD65

CC (R59517) were determined. New soluble fragments of GAD65

CC (R59518-25) were prepared by deletion/substitution

CC mutagenesis. These fragments are free of N-terminal amino acids

CC that limit solubility. Different fragments contain epitopes for

CC different classes of GAD65 autoantibodies.

CC Sequence 554 AA;

SQ

Query Match 100.0%; Score 147; DB 1; Length 554;  
 Best Local Similarity 100.0%; Pred. No. 3.73e-09;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 135 TLKYAIKTGHPRYFNQSTG 154  
 |||||  
 QY 1 TLKYAIKTGHPRYFNQSTG 20

RESULT 10  
 ID W34520 standard; protein; 584 AA.  
 AC W34520:  
 DT 24-MAR-1998 (first entry)  
 DE Rat GAD65 protein.  
 KW GAD65; glutamic acid decarboxylase protein; rat; soluble fragment;  
 autoantibody; insulin-dependent diabetes mellitus; IDDM; diagnosis;  
 KW stiff man syndrome; therapy.  
 OS Rattus sp.  
 PN US5691448-A.  
 PD 25-NOV-1997.  
 PF 02-DEC-1993; 161290.  
 PR 02-DEC-1993; US-161290.  
 PR 03-DEC-1992; US-984935.  
 PA (BAEK/) BAEKESKOV S.  
 PA (KIMJ/) KIM J.  
 PA (NAMC/) NAMCHUK M.  
 PA (RICH/) RICHTER W.  
 PA (SHIY/) SHI Y.  
 PI Baekeskov S, Kim J, Namchuk M, Richter W, Shi Y;  
 DR WPI: 98-017711/02.  
 PT Soluble fragments of glutamic acid decarboxylase GAD65 - used to  
 distinguish between insulin-dependent diabetes mellitus and  
 stiff man syndrome  
 PS This sequence represents the rat glutamic acid decarboxylase protein  
 disclosure; column 31-34: 30pp; English.  
 CC This sequence relates to soluble fragments of a GAD65 protein that  
 are specifically reactive with a GAD65 autoantibody (AAb), where the  
 fragment is at least 98% pure and the AAb binds to a conformational  
 epitope of the fragment. The soluble GAD65 fragments can be used to  
 distinguish between insulin-dependent diabetes mellitus (IDDM) and stiff  
 man syndrome. They can also be used for diagnosis and treatment of IDDM  
 CC and stiff man syndrome. The fragments can distinguish different temporal  
 stages in the progression of IDDM.  
 CC Sequence 584 AA;  
 SQ

Query Match 100.0%; Score 147; DB 1; Length 584;  
 Best Local Similarity 100.0%; Pred. No. 3.73e-09;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 166 TLKYAIKTGHPRYFNQSTG 185  
 |||||  
 QY 1 TLKYAIKTGHPRYFNQSTG 20

RESULT 11  
 ID W86018 standard; protein; 584 AA.  
 AC W86018:  
 DT 22-FEB-1999 (first entry)  
 DE Rat GAD65 protein sequence.  
 KW GAD65; autoantibody; soluble; detection; diagnosis; monitor; IDDM;  
 insulin-dependent diabetes mellitus; stiff man syndrome.  
 OS Rattus sp.  
 PN US5849506-A.  
 PD 15-DEC-1998.  
 PF 25-MAY-1995; 450755.  
 PR 02-DEC-1993; US-161290.  
 PR 03-DEC-1992; US-984935.  
 PR 25-MAY-1995; US-450755.  
 PA (RECC) UNIV CALIFORNIA.  
 PI Baekeskov S, Kim J, Namchuk M, Richter W, Shi Y;  
 DR WPI: 99-069720/06.  
 PT Immunoassay for GAD65 auto-antibodies - used for diagnosis of  
 diabetes and stiff man syndrome

PS Examples; Fig 1; 31pp; English.  
 CC This represents a human GAD65 protein sequence. The invention provides  
 CC soluble fragments of GAD65 that are specifically reactive with at least  
 CC one class of GAD65 autoantibody. The fragments are substantially free of  
 CC N-terminal amino acids that would otherwise limit solubility. Different  
 CC fragments contain different epitopes for different classes of GAD65  
 CC autoantibodies. These fragments are used in the methods of the invention  
 CC for detection of GAD65 autoantibodies. The methods are used for  
 CC diagnosing or monitoring insulin-dependent diabetes mellitus (IDDM) and  
 CC stiff man syndrome.  
 SQ Sequence 584 AA;

Query Match 100.0%; Score 147; DB 1; Length 584;  
 Best Local Similarity 100.0%; Pred. No. 3.73e-09;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 166 TLKYAIKTGHPRYFNQSTG 185  
 |||||  
 QY 1 TLKYAIKTGHPRYFNQSTG 20

RESULT 12  
 ID W86017 standard; protein; 584 AA.  
 AC W86017:  
 DT 22-FEB-1999 (first entry)  
 DE Human GAD65 protein sequence.  
 KW GAD65; autoantibody; soluble; detection; diagnosis; monitor; IDDM;  
 KW insulin-dependent diabetes mellitus; stiff man syndrome.  
 OS Homo sapiens.  
 PN US5849506-A.  
 PD 15-DEC-1998.  
 PF 25-MAY-1995; 450755.  
 PR 02-DEC-1993; US-161290.  
 PR 03-DEC-1992; US-984935.  
 PR 25-MAY-1995; US-450755.  
 PA (RECC) UNIV CALIFORNIA.  
 PI Baekeskov S, Kim J, Namchuk M, Richter W, Shi Y;  
 DR WPI: 99-069720/06.  
 PT Immunoassay for GAD65 auto-antibodies - used for diagnosis of  
 PT diabetes and stiff man syndrome  
 PS Examples; Fig 1; 31pp; English.  
 CC This represents a human GAD65 protein sequence. The invention provides  
 CC soluble fragments of GAD65 that are specifically reactive with at least  
 CC one class of GAD65 autoantibody. The fragments are substantially free of  
 CC N-terminal amino acids that would otherwise limit solubility. Different  
 CC fragments contain different epitopes for different classes of GAD65  
 CC autoantibodies. These fragments are used in the methods of the invention  
 CC for detection of GAD65 autoantibodies. The methods are used for  
 CC diagnosing or monitoring insulin-dependent diabetes mellitus (IDDM) and  
 CC stiff man syndrome.  
 SQ Sequence 584 AA;

Query Match 100.0%; Score 147; DB 1; Length 584;  
 Best Local Similarity 100.0%; Pred. No. 3.73e-09;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 166 TLKYAIKTGHPRYFNQSTG 185  
 |||||  
 QY 1 TLKYAIKTGHPRYFNQSTG 20

RESULT 13  
 ID W34519 standard; protein; 584 AA.  
 AC W34519:  
 DT 24-MAR-1998 (first entry)  
 DE Human GAD65 protein.  
 KW GAD65; glutamic acid decarboxylase protein; human; soluble fragment;  
 KW autoantibody; insulin-dependent diabetes mellitus; IDDM; diagnosis;  
 KW stiff man syndrome; therapy.  
 OS Homo sapiens.  
 PN US5691448-A.  
 PD 25-NOV-1997.  
 PF 02-DEC-1993; 161290.



PR 02-DEC-1993: US-161290.  
 PR 03-DEC-1992: US-984935.  
 PA (BAEK/) BAEKESKOV S.  
 PA (KIMJ/) KIM J.  
 PA (NAMC/) NAMCHUK M.  
 PA (RICH/) RICHTER W.  
 PA (SHIY/) SHI Y.  
 PI Baekeskov S, Kim J, Namchuk M, Richter W, Shi Y;  
 PI WPI: 98-017711/02.  
 PT Soluble fragments of glutamic acid decarboxylase GAD65 - used to  
 PT distinguish between insulin-dependent diabetes mellitus and  
 PT stiff-man syndrome  
 PS Disclosure: column 27-30; 30pp; English.  
 CC This sequence represents the human glutamic acid decarboxylase protein  
 CC GAD65. The invention relates to soluble fragments of a GAD65 protein that  
 CC are specifically reactive with a GAD65 autoantibody (AAb), where the  
 CC fragment is at least 9% pure and the AAb binds to a conformational  
 CC epitope of the fragment. The soluble GAD65 fragments can be used to  
 CC distinguish between insulin-dependent diabetes mellitus (IDDM) and stiff  
 CC man syndrome. They can also be used for diagnosis and treatment of IDDM  
 CC and stiff man syndrome. The fragments can distinguish different temporal  
 CC stages in the progression of IDDM.  
 SQ Sequence 584 AA;

Query Match 100.0%; Score 147; DB 1; Length 584;  
 Best Local Similarity 100.0%; Pred. No. 3.73e-09;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 166 TLKAIKTHGHPRYFNOLSTG 185  
 OY 1 TLKAIKTHGHPRYFNOLSTG 20

RESULT 14  
 ID R79105 standard: Protein: 585 AA.  
 AC R79105: 13-NOV-1995 (first entry)  
 DE Human glutamic acid decarboxylase (GAD65).  
 KM Rat glutamic acid decarboxylase; GAD65; autoimmune disorders;  
 KM Insulin-dependent diabetes mellitus; stiff man disease.  
 OS Homo sapiens.  
 PN W09507992-A.  
 PD 23-MAR-1995.  
 PR 24-AUG-1994: U09478.  
 PR 17-SEP-1993: US-123859.  
 PA (REGC ) UNIV CALIFORNIA.  
 PI Clare-Salzler MJ, Erlander MG, Kaufman DL, Tobin AJ;  
 PI WPI: 95-131360/17.  
 DR N-PSDB: Q86482.  
 PT New polypeptide fragments of glutamic acid decarboxylase - for  
 PT diagnosis and treatment of autoimmune disease; esp. insulin  
 PT dependent diabetes; also related nucleic acid, vectors,  
 PT antibodies, hybridoma(s) etc.  
 PS Example 1: Fig 3; 10pp; English.  
 CC Q86481 and Q86482 encode R71733 and R79105, rat and human glutamic  
 CC acid decarboxylase (GAD65) respectively, from which the GAD65  
 CC fragments described in R72261-R72298 were derived. These fragments  
 CC can be used to detect autoantibodies against GAD, e.g. to diagnose  
 CC and treat GAD-related autoimmune disorders, such as insulin  
 CC dependant diabetes mellitus or stiff man disease.  
 SQ Sequence 585 AA;

Query Match 100.0%; Score 147; DB 1; Length 585;  
 Best Local Similarity 100.0%; Pred. No. 3.73e-09;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 166 TLKAIKTHGHPRYFNOLSTG 185  
 OY 1 TLKAIKTHGHPRYFNOLSTG 20

RESULT 15  
 ID W14915 standard: Protein: 585 AA.

AC W14915;  
 DT 10-JUL-1997 (first entry)  
 DE Modified glutamic acid decarboxylase (K396R).  
 KM Glutamic acid decarboxylase; GAD; autoimmune disease; therapy;  
 KM Insulin-dependent diabetes mellitus; vaccine;  
 KW enzyme engineering; protein engineering.  
 OS Synthetic.  
 PN W09712034-A1.  
 PD 03-APR-1997.  
 PE 27-SEP-1996: SE1210.  
 PR 28-SEP-1995: SE-003379.  
 PA (SYNE-) SYNECTICS BIOTECHNOLOGY AB.  
 PI Essen-Moeller A, Falorni A, Lermarck A, Robertson J;  
 PI WPI: 97-212895/19.  
 DR N-PSDB: T64560.  
 PT Modified glutamic acid decarboxylase for autoimmune disease  
 PT treatment - has immunoreactivity of unmodified GAD65 but decreased  
 PT enzyme activity, esp. useful for insulin-dependent diabetes mellitus  
 PT treatment  
 PS Claim 3: Page 13-15; 24pp; English.  
 CC A modified human glutamic acid decarboxylase (GAD) (W14915) has the  
 CC native lysine residue at amino acid position 396 replaced by  
 CC arginine. It is obtd. by site-directed mutagenesis (see also  
 CC T64561) of native human GAD65 cDNA and expression of the mutant DNA  
 CC (T64560) in transformed host cells. Lys-396 is critical for enzyme  
 CC activity. By replacing it with an amino acid incapable of Schiff  
 CC base formation, immunoreactivity is maintained but enzyme activity  
 CC is reduced or lost, so minimising the risk of toxicity. The  
 CC modified GAD can be used to treat and/or prevent autoimmune  
 CC disorders such as insulin-dependent diabetes mellitus (IDDM) and  
 CC other diseases, e.g. neurological diseases, esp. in individuals  
 CC having a genetic predisposition for IDDM or with an increased  
 CC antibody titre against GAD.  
 SQ Sequence 585 AA;

Query Match 100.0%; Score 147; DB 1; Length 585;  
 Best Local Similarity 100.0%; Pred. No. 3.73e-09;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 166 TLKAIKTHGHPRYFNOLSTG 185  
 OY 1 TLKAIKTHGHPRYFNOLSTG 20

Search completed: Tue Mar 7 21:35:55 2000  
 Job time : 4 secs.

**THIS PAGE BLANK (USPTO)**

\*\*\*\*\*  
[W][O][R][D] (TM)  
\*\*\*\*\*

Release 3.1a John F. Collins, Biocomputing Research Unit.  
Copyright (c) 1993-1998 University of Edinburgh, U.K.  
Distribution rights by Oxford Molecular Ltd

MSrch\_PP protein - protein database search, using Smith-Waterman algorithm  
Run on: Tue Mar 7 21:35:25 2000; Maspar time 5.65 Seconds  
166,906 Million cell updates/sec  
Tabular output not generated.

Title: >US-08-981-824-4  
Description: (1-20) from US08981824.pep  
Perfect Score: 147  
Sequence: 1 TLKYAIKTHPRFYNQSTG 20

Scoring table: PAM 150  
Gap 15

Searched: 142080 seqs, 47172406 residues

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: p162  
1:p1r1 2:p1r2 3:p1r3 4:p1r4

Statistics: Mean=28.585; Variance 41.506; scale 0.689

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	147	100.0	585	2 JC4064	glutamate decarboxyla	1.16e-18
2	147	100.0	585	1 A41292	glutamate decarboxyla	1.16e-18
3	147	100.0	585	1 J38533	glutamate decarboxyla	1.16e-18
4	147	100.0	585	1 JH0423	glutamate decarboxyla	1.16e-18
5	134	91.2	223	2 T59173	glutamate decarboxyla	1.62e-15
6	134	91.2	585	2 S61534	glutamate decarboxyla	1.62e-15
7	134	91.2	593	1 A41367	glutamate decarboxyla	1.62e-15
8	134	91.2	593	2 S48135	glutamate decarboxyla	1.62e-15
9	134	91.2	593	2 S41775	glutamate decarboxyla	1.62e-15
10	134	91.2	594	1 B41935	glutamate decarboxyla	1.62e-15
11	134	91.2	594	2 JC4065	glutamate decarboxyla	1.62e-15
12	134	91.2	594	2 S51775	glutamate decarboxyla	1.62e-15
13	134	91.2	594	1 A46758	glutamate decarboxyla	1.62e-15
14	133	93.7	510	1 A30999	glutamate decarboxyla	6.52e-13
15	108	73.5	493	2 S71489	glutamate decarboxyla	1.83e-09
16	87	59.2	575	1 JH0827	glutamate decarboxyla	6.66e-05
17	85	57.8	205	2 I67412	65 kDa glutamate deca	1.73e-04
18	69	46.9	413	2 DEUS08	hypothetical protein	2.38e-01
19	68	46.3	391	1 DEUS08	dihydroorotase (EC 3.	3.64e-01
20	68	46.3	1224	2 T00059	hypothetical protein	3.64e-01
21	65	44.2	764	2 S49849	aconitate hydratase	1.27e+00
22	65	44.2	898	2 T04693	aconitate hydratase	1.27e+00
23	64	43.5	475	2 F64151	hypothetical protein	1.91e+00

24	63	42.9	90	2 H64649	ribosomal protein S15	2.87e+00
25	63	42.9	368	2 I80811	histone H2A.1 - rat	2.87e+00
26	62	42.2	266	2 B70872	4-phosphate ABC-type tra	4.28e+00
27	61	41.5	112	2 B72019	periplasmic divalent	6.36e+00
28	61	41.5	260	2 S72767	probable ABC transport	6.36e+00
29	61	41.5	286	1 A45350	matrix protein ML - S	6.36e+00
30	61	41.5	293	2 T04951	hypothetical protein	6.36e+00
31	61	41.5	373	2 S39722	spore coat polysaccha	6.36e+00
32	61	41.5	726	2 T16355	hypothetical protein	6.36e+00
33	61	41.5	1787	2 D69195	protoporphyrin IX mag	6.36e+00
34	60	40.8	301	2 JC5846	chitinase (EC 3.2.1.1	9.41e+00
35	60	40.8	339	2 S17930	transcription initiat	9.41e+00
36	60	40.8	567	2 T16625	hypothetical protein	9.41e+00
37	59	40.1	90	2 F71937	ribosomal protein S15	1.39e+01
38	59	40.1	185	2 F64878	aldehyde dehydrogenas	1.39e+01
39	59	40.1	201	2 D36838	D13L protein - variol	1.39e+01
40	59	40.1	221	2 B70348	hypothetical protein	1.39e+01
41	59	40.1	297	2 T09311	hypothetical protein	1.39e+01
42	59	40.1	616	2 T07611	immediate-early prote	1.39e+01
43	59	40.1	644	2 A72519	aconitate hydratase	1.39e+01
44	59	40.1	862	2 S64821	probable 2-oxoacid-1	1.39e+01
45	58	39.5	289	2 E71939	probable membrane pro	2.03e+01
					hypothetical protein	2.03e+01

## ALIGNMENTS

RESULT	1	ALIGNMENTS
ENTRY	JC4064	#type complete
TITLE	glutamate decarboxylase (EC 4.1.1.15) 65k chain - pig	
ORGANISM	#formal_name Sus scrofa domestica #common_name domestic pig	
DATE	30-Jun-1995 #sequence_revision 14-Jul-1995 #text_change 22-Jun-1999	
ACCESSIONS	JC4064	
REFERENCE	JC4064	
#authors	Suzuki, R.; Asami, N.; Amann, E.; Magatsuna, M.	
#journal	Gene (1995) 152:257-260	
#title	Sequences of two porcine glutamic acid decarboxylases (65- and 67-kDa GAD).	
#cross-references	MOLID:95137399	
#accession	JC4064	
#molecule_type	mrna	
#residues	1-585 #label S02	
#cross-references	DDI:D31846; NID:9790964; PIDN:BA00693.1; PID:d1007207; PID:g90965	
COMMENT	#experimental_source brain This enzyme catalyzes the conversion of glutamic acid into gamma-amino butyric acid.	
CLASSIFICATION	#superfamily human glutamate decarboxylase	
KEYWORDS	carbon-carbon lyase; carboxy-lyase	
FEATURE		
393-396	#domain DOPA decarboxylase binding #status predicted	
SUMMARY	#length 585 #molecular-weight 65388 #checksum 5933	
Query Match	100.0%; Score 147; DB 2; Length 585;	
Best Local Similarity	100.0%; Pred. No. 1.16e-18;	
Matches	20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Db	166 TLKYAIKTHPRFYNQSTG 185	
Qy	1 TLKYAIKTHPRFYNQSTG 20	
RESULT	2	
ENTRY	A41292	#type complete
TITLE	glutamate decarboxylase (EC 4.1.1.15) 2 - human	
ALTERNATE_NAMES	glutamate decarboxylase GAD65; L-glutamate 1-carboxy-lyase	
ORGANISM	#formal_name Homo sapiens #common_name man	
DATE	13-May-1992 #sequence_revision 23-Mar-1995 #text_change 18-Jun-1999	
ACCESSIONS	A41935; A41292; S30058; B54778	
REFERENCE	A41935	
#authors	Bu, D.F.; Eriander, M.G.; Hltz, B.C.; Tiliakaratne, N.J.K.;	

Kaufman, D.L.; Wagner-McPherson, C.B.; Evans, G.A.; Tobin, A.J.  
 #journal Proc. Natl. Acad. Sci. U.S.A. (1992) 89:2115-2119  
 #title Two human glutamate decarboxylases, 65-kDa GAD and 67-kDa GAD, are each encoded by a single gene.  
 #cross-references MUID:92196068  
 #accession A41935  
 ##molecule-type mRNA  
 ##residues 1-585 ##label BUI  
 ##cross-references GB:M81882; NID:9182933; PIDN:AAA62367.1; PID:9182934  
 ##experimental\_source brain  
 ##note sequence extracted from NCBI backbone (NCBI:P:88007)  
 REFERENCE  
 #authors Karlisen, A.E.; Hagopian, W.A.; Grubbin, C.E.; Dube, S.; Distcheche, C.M.; Adler, D.A.; Baermeier, H.; Mathewes, S.; Grant, F.J.; Foster, D.; Lermack, A.  
 #journal Proc. Natl. Acad. Sci. U.S.A. (1991) 88:8337-8341  
 #title Cloning and primary structure of a human islet isoform of glutamic acid decarboxylase from chromosome 10.  
 #cross-references MUID:92020848  
 #accession A41292  
 ##molecule-type mRNA  
 ##residues 1-585 ##label KAR  
 ##cross-references GB:M74826; NID:9182931; PIDN:AAA58491.1; PID:9182932  
 ##experimental\_source pancreatic islet  
 REFERENCE  
 #authors Mauch, L.; Abney, C.C.; Berg, H.; Scherbaum, W.A.; Liedvogel, B.; Northemann, W.  
 #journal Eur. J. Biochem. (1993) 212:597-603  
 #title Characterization of a linear epitope within the human pancreatic 64-kDa glutamic acid decarboxylase and its autoimmunity recognition by sera from insulin-dependent diabetes mellitus patients.  
 #cross-references MUID:93185681  
 #accession S30058  
 ##molecule-type mRNA  
 ##residues 6-585 ##label MAU  
 ##cross-references EMBL:X69936  
 ##experimental\_source pancreatic islet  
 REFERENCE  
 #authors Bu, D.F.; Tobin, A.J.  
 #journal Genomics (1994) 21:222-228  
 #title The exon-intron organization of the genes (GAD1 and GAD2) encoding two human glutamate decarboxylases (GAD-67 and GAD-65) suggests that they derive from a common ancestral GAD.  
 #cross-references MUID:94375018  
 #contents annotation; intron-exon boundaries  
 #COMMENT This enzyme (GAD) catalyzes the formation of an inhibitory neurotransmitter, gamma-aminobutyric acid, from L-glutamic acid; it has several isoforms, each encoded by a separate gene. GAD has also been implicated as an autoantigen in autoimmune disease stiff-man syndrome and insulin-dependent diabetes mellitus.  
 GENETICS  
 #gene GDB:GAD2  
 ##cross-references GDB:128595; OMIM:138275  
 #map\_position 10p11.23-10p11.23  
 CLASSIFICATION  
 #superfamily human glutamate decarboxylase  
 #keywords carbon-carbon lyase; carboxy-lyase; phosphoprotein; pyridoxal phosphate  
 FEATURE  
 #396 #binding-site pyridoxal phosphate (lys) (covalent)  
 #status predicted  
 #length 585 #molecular-weight 65411 #checksum 4799  
 SUMMARY  
 #length 585 #molecular-weight 65411 #checksum 4799  
 Query Match 100.0%; Score 147; DB 1; Length 585;  
 Best Local Similarity 100.0%; Pred. No. 1,16e-18;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Db 166 TLKAIKTGHPRYNQLSTG 185  
 1 TLKAIKTGHPRYNQLSTG 20

RESULT 3  
 ENTRY S38533 #type complete  
 TITLE glutamate decarboxylase (EC 4.1.1.15) 2 - mouse  
 ALTERNATE\_NAMES glutamate decarboxylase GAD65; L-glutamate 1-carboxy-lyase  
 ORGANISM #formal\_name Mus musculus #common\_name house mouse  
 DATE 20-May-1994 #sequence\_revision 23-Mar-1995 #text\_change 18-Jun-1999  
 ACCESSIONS S38533  
 REFERENCE S38533  
 #authors Lee, D.S.; Tian, J.; Phan, T.; Kaufman, D.L.  
 #journal Biochim. Biophys. Acta (1993) 1216:157-160  
 #title Cloning and sequence analysis of a murine cDNA encoding glutamate decarboxylase (GAD65).  
 #cross-references MUID:94032481  
 #accession S38533  
 ##status preliminary  
 ##molecule-type mRNA  
 ##residues 1-585 ##label LEE  
 ##cross-references GB:L16980; NID:9413867; PIDN:AAA93049.1; PID:9413868  
 #COMMENT This enzyme (GAD) catalyzes the formation of an inhibitory neurotransmitter, gamma-aminobutyric acid, from L-glutamic acid; it has several isoforms, each encoded by a separate gene.  
 CLASSIFICATION  
 #superfamily human glutamate decarboxylase  
 #keywords carbon-carbon lyase; carboxy-lyase; phosphoprotein; pyridoxal phosphate  
 FEATURE  
 #396 #binding-site pyridoxal phosphate (lys) (covalent)  
 #status predicted  
 #length 585 #molecular-weight 65224 #checksum 7599  
 SUMMARY  
 #length 585 #molecular-weight 65224 #checksum 7599  
 Query Match 100.0%; Score 147; DB 1; Length 585;  
 Best Local Similarity 100.0%; Pred. No. 1,16e-18;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Db 166 TLKAIKTGHPRYNQLSTG 185  
 1 TLKAIKTGHPRYNQLSTG 20

RESULT 4  
 ENTRY JH0423 #type complete  
 TITLE glutamate decarboxylase (EC 4.1.1.15) 2 - rat  
 ALTERNATE\_NAMES glutamate decarboxylase GAD65; L-glutamate 1-carboxy-lyase  
 ORGANISM #formal\_name Rattus norvegicus #common\_name Norway rat  
 DATE 31-Mar-1992 #sequence\_revision 23-Mar-1995 #text\_change 18-Jun-1999  
 ACCESSIONS JH0423; A60888  
 REFERENCE JH0423  
 #authors Erlander, M.G.; Tillakaratne, N.U.K.; Feldblum, S.; Patel, N.; Tobin, A.J.  
 #journal Neuron (1991) 7:91-100  
 #title Two genes encode distinct glutamate decarboxylases.  
 #cross-references MUID:91299343  
 #accession JH0423  
 ##molecule-type mRNA  
 ##residues 1-585 ##label ERL  
 ##cross-references GB:M72422; NID:9204225; PIDN:AAA63488.1; PID:9204226  
 ##experimental\_source brain  
 ##note the authors translated the codon GAT for residue 86 as His, TCA for residue 198 as Ala, and CAG for residue 428 as Trp  
 REFERENCE  
 #authors A60888  
 #journal Chang, Y.C.; Gottlieb, D.I.  
 #journal J. Neurosci. (1988) 8:2123-2130  
 #title Characterization of the proteins purified with monoclonal antibodies to glutamic acid decarboxylase.  
 #cross-references MUID:88258610  
 #accession A60888  
 ##status preliminary  
 ##molecule-type protein  
 ##residues 191-194, 'X', 196-203, 'XX', 206-219, 'X', 225-234, 'X', 236-247, 'X', 249-266, 'X', 524-537, 539-543, 'V', 547-549,

COMMENT This enzyme (GAD) catalyzes the formation of an inhibitory neurotransmitter, gamma-aminobutyric acid, from L-glutamic acid. It has several isoforms, each encoded by a separate gene.

CLASSIFICATION #superfamily human glutamate decarboxylase

KEYWORDS carbon-carbon lyase; carboxy-lyase; phosphoprotein; pyridoxal phosphate

FEATURE 396 #binding-site pyridoxal phosphate (Lys) (covalent)  
#status predicted

SUMMARY #length 585 #molecular-weight 65402 #checksum 7756

Query Match 100.0%: Score 147; DB 1; Length 585;  
Best Local Similarity 100.0%: Pred. No. 1.16e-18;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 166 TLKXKRTGHPHFNOI185  
1 TLKXKRTGHPHFNOI185

QY 1 TLKXKRTGHPHFNOI185

RESULT 5

ENTRY 159173 #type complete

TITLE glutamate decarboxylase - rat

ALTERNATE\_NAMES #formal\_name Rattus norvegicus #common\_name Norway rat

ORGANISM 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change

DATE 22-Jun-1999

ACCESSIONS 159173

REFERENCE Bond, R.W.; Wyborski, R.J.; Gottlieb, D.I.  
Proc. Natl. Acad. Sci. U.S.A. (1990) 87:8771-8775

#authors #journal Developmentally regulated expression of an exon containing a stop codon in the gene for glutamic acid decarboxylase.

#title

#cross-references MUID:91062362

#accession 159173

#status preliminary; translated from GB/EMBL/DBJ

#molecule\_type mRNA

#residues 1-223 #label RES

CLASSIFICATION #cross-references GB:M38350; NID:9204231; PIDN:AAA1185.1; PID:9204232

SUMMARY #superfamily human glutamate decarboxylase  
#length 223 #molecular-weight 25069 #checksum 1388

Query Match 91.2%: Score 134; DB 2; Length 223;  
Best Local Similarity 80.0%: Pred. No. 1.62e-15;  
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Db 174 TLKXGRTGHPHFNOI193  
1 TLKXKRTGHPHFNOI193

QY 1 TLKXKRTGHPHFNOI193

RESULT 6

ENTRY 561534 #type complete

TITLE glutamate decarboxylase (EC 4.1.1.15) 62k isoform - mouse

ALTERNATE\_NAMES glutamic acid decarboxylase

ORGANISM #formal\_name Mus musculus #common\_name house mouse

DATE 19-Mar-1997 #sequence\_revision 25-Apr-1997 #text\_change

ACCESSIONS 561534

REFERENCE Katarova, Z.; Szabo, G.; Mugnaini, E.; Greenspan, R.J.  
Eur. J. Neurosci. (1990) 2:190-202

#authors #journal Molecular identification of the 62 kd form of glutamic acid decarboxylase from the mouse.

#title

#accession 561534

#molecule\_type mRNA

#residues 1-585 #label KAT

CLASSIFICATION #cross-references EMBL:249976

KEYWORDS #experimental\_source brain

REFERENCE 561533

#authors Szabo, G.

#submission submitted to the EMBL Data Library, June 1995

#accession 561533

#molecule\_type mRNA

#residues 1-534, 'YOPQGDKNFFRMVSNPASOSDIDFTEIERLGQDL' #label SZA

#cross-references EMBL:249976; NID:9886686; PIDN:CAA90277.1; PID:9886687

#experimental\_source brain

#note the differences at the carboxyl end are due to a frameshift error

CLASSIFICATION #superfamily human glutamate decarboxylase

KEYWORDS carbon-carbon lyase; carboxy-lyase

SUMMARY #length 585 #molecular-weight 65381 #checksum 5716

Query Match 91.2%: Score 134; DB 2; Length 585;  
Best Local Similarity 80.0%: Pred. No. 1.62e-15;  
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Db 174 TLKXGRTGHPHFNOI193  
1 TLKXKRTGHPHFNOI193

QY 1 TLKXKRTGHPHFNOI193

RESULT 7

ENTRY 441367 #type complete

TITLE glutamate decarboxylase (EC 4.1.1.15) 1 - rat

ALTERNATE\_NAMES glutamate decarboxylase GAD67; L-glutamate 1-carboxy-lyase

ORGANISM #formal\_name Rattus norvegicus #common\_name Norway rat

DATE 12-Jun-1992 #sequence\_revision 23-Mar-1995 #text\_change

ACCESSIONS 441367; A43756; JH0195

REFERENCE 441367; A43756; JH0195

#authors Michelsen, B.K.; Petersen, J.S.; Boel, E.; Moldrup, A.; Dyrberg, T.; Madsen, O.D.  
Proc. Natl. Acad. Sci. U.S.A. (1991) 88:8754-8758

#journal Cloning, characterization, and autoimmune recognition of rat islet glutamic acid decarboxylase in insulin-dependent diabetes mellitus.

#title

#cross-references MUID:92020930

#accession 441367

#status preliminary

#molecule\_type mRNA

#residues 1-593 #label MIC

REFERENCE 443756

#authors Wyborski, R.J.; Bond, R.W.; Gottlieb, D.I.  
Brain Res. Mol. Brain Res. (1990) 8:193-198

#journal Characterization of a cDNA coding for rat glutamic acid decarboxylase.

#title

#cross-references MUID:91014554

#accession A43756

#status preliminary

#molecule\_type mRNA

#residues 1-593 #label WYB

#cross-references GB:X57573; NID:956183; PIDN:CAA0801.1; PID:956184

#note the authors translated the codon TGT for residue 412 as Ser and TCT for residue 413 as Cys

REFERENCE JH0195

#authors Julien, J.F.; Samama, P.; Mallet, J.  
J. Neurochem. (1990) 54:703-705

#journal Rat brain glutamic acid decarboxylase sequence deduced from a cloned cDNA.

#title

#cross-references MUID:90132703

#accession JH0195

#molecule\_type mRNA

#residues 1-102, 'V', 104-283, 'S', 285-286, 'AD', 289-343, 'EA', 346, 'I', 348-351, 'LE', 354-379, 'R', 381-593 #label JUL

CLASSIFICATION #cross-references GB:X57572; NID:956185; PIDN:CAA0800.1; PID:956186

COMMENT This enzyme (GAD) catalyzes the formation of an inhibitory neurotransmitter, gamma-aminobutyric acid, from L-glutamic acid. It has several isoforms, each encoded by a separate gene.

CLASSIFICATION #superfamily human glutamate decarboxylase

KEYWORDS carbon-carbon lyase; carboxy-lyase; phosphoprotein; pyridoxal phosphate

FEATURE

404 #binding\_site pyridoxal phosphate (Lys) (covalent)  
#status predicted  
SUMMARY #length 593 #molecular-weight 66640 #checksum 3971

Query Match 91.2%: Score 134; DB 1; Length 593;  
Best Local Similarity 80.0%: Pred. No. 1.62e-15;  
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Db 174 TLKYGVRTGHPREFNOLSTG 193  
1 TLKYAIKTGHPREFNOLSTG 20

RESULT 8  
ENTRY S48135 #type complete  
TITLE glutamate decarboxylase (EC 4.1.1.15) - human  
ORANISM #formal\_name Homo sapiens #common\_name man  
DATE 14-Jul-1995 #sequence\_revision 10-Nov-1995 #text\_change 07-May-1999

ACCESSIONS S48135  
REFERENCE S48135  
#authors Kelly, C.D.; Edwards, Y.; Johnstone, A.P.; Harfst, E.; Nogradi, A.; Nussey, S.S.; Povey, S.; Carter, N.D.  
#journal Ann. Hum. Genet. (1992) 56:255-265  
#title Nucleotide sequence and chromosomal assignment of a cDNA encoding the large isoform of human glutamate decarboxylase.  
#cross-references M01D:93080286  
#accession S48135  
#molecule\_type mRNA  
#residues 1-593 #label KEL

CLASSIFICATION #superfamily human glutamate decarboxylase  
KEYWORDS #carbon-carbon lyase; carboxy-lyase  
SUMMARY #length 593 #molecular-weight 66952 #checksum 4836

Query Match 91.2%: Score 134; DB 2; Length 593;  
Best Local Similarity 80.0%: Pred. No. 1.62e-15;  
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Db 174 TLKYGVRTGHPREFNOLSTG 193  
1 TLKYAIKTGHPREFNOLSTG 20

RESULT 9  
ENTRY S51776 #type complete  
TITLE glutamate decarboxylase (EC 4.1.1.15) - human  
ORANISM #formal\_name Homo sapiens #common\_name man  
DATE 15-Jul-1995 #sequence\_revision 21-Jul-1995 #text\_change 16-Feb-1997

ACCESSIONS S51776  
REFERENCE S51775  
#authors Johnstone, A.  
#submission submitted to the EMBL Data Library, May 1993  
#accession S51776  
#status preliminary  
#molecule\_type mRNA  
#residues 1-593 #label JOH  
#cross-references EMBL:223750  
#note this is an unpublished revision to the sequence from reference S48135

CLASSIFICATION #superfamily human glutamate decarboxylase  
KEYWORDS #carbon-carbon lyase; carboxy-lyase  
SUMMARY #length 593 #molecular-weight 66946 #checksum 4842

Query Match 91.2%: Score 134; DB 2; Length 593;  
Best Local Similarity 80.0%: Pred. No. 1.62e-15;  
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Db 174 TLKYGVRTGHPREFNOLSTG 193  
1 TLKYAIKTGHPREFNOLSTG 20

RESULT 10  
ENTRY B41935 #type complete  
TITLE glutamate decarboxylase (EC 4.1.1.15) 1 - human  
ALTERNATE\_NAMES glutamate decarboxylase GAD67; L-glutamate 1-carboxy-lyase  
ORANISM #formal\_name Homo sapiens #common\_name man  
DATE 31-Dec-1993 #sequence\_revision 23-Mar-1995 #text\_change 18-Jun-1999

ACCESSIONS B41935; JH0805; A61406; P00157; P00158; B41367;  
A36463; A54778  
REFERENCE B41935  
#authors Bu, D.F.; Erlander, M.G.; Hitz, B.C.; Tiliakaratne, N.J.K.; Kaufman, D.L.; Wagner-McPherson, C.B.; Evans, G.A.; Tobin, A.J.  
#journal Proc. Natl. Acad. Sci. U.S.A. (1992) 89:2115-2119  
#title Two human glutamate decarboxylases, 65-kDa GAD and 67-kDa GAD, are each encoded by a single gene.  
#cross-references M01D:92196068  
#accession B41935  
#molecule\_type mRNA  
#residues 1-594 #label BU1  
#cross-references GB:881883; NID:q182935; PIDN:AAA62368.1; PID:q182936  
#experimental\_source pancreatic islet  
#note sequence extracted from NCBI backbone (NCBIF:88006)

REFERENCE JH0805  
#authors Kawasaki, E.; Moriwaki, R.; Watanabe, M.; Saitoh, K.; Charles Brunicaudi, F.; Watt, P.C.; Yamaguchi, T.; Mullen, Y.; Akazawa, S.; Miyamoto, T.; Nagataki, S.  
#journal Biochem. Biophys. Res. Commun. (1993) 192:1353-1359  
#title Cloning and expression of large isoform of glutamic acid decarboxylase from human pancreatic islet.  
#cross-references M01D:93282845  
#accession JH0805  
#molecule\_type mRNA  
#residues 1-17, 'N', 19-30, 'N', 32-67, 'K', 69-115, 'L', 117-154, 'T', 156-301, 'C', 303-476, 'G', 478-491, 'G', 493-594 #label KAW

#cross-references GB:561898; NID:q385310; PIDN:AA826938.1; PID:q385311  
#experimental\_source pancreatic islet  
REFERENCE JH0806  
#authors Yamashita, K.; Cram, D.S.; Harrison, L.C.  
#journal Biochem. Biophys. Res. Commun. (1993) 192:1347-1352  
#title Molecular cloning of full-length glutamic acid decarboxylase 67 from human pancreas and islets.  
#cross-references M01D:93282844  
#accession JH0806  
#molecule\_type mRNA  
#residues 1-67, 'K', 69-435, 'L', 437-511, 'S', 513-594 #label YAM

#cross-references GB:561897; NID:q385450; PIDN:AA826937.1; PID:q385451  
#experimental\_source pancreatic islet  
REFERENCE A61406  
#authors Kelly, C.; Carter, N.D.; Johnstone, A.P.; Nussey, S.S.  
#journal Lancet (1991) 338:1468-1469  
#title Cloning of large isoform of human brain glutamic acid decarboxylase.  
#cross-references M01D:92065769  
#accession A61406  
#molecule\_type mRNA  
#residues 62-67, 'K', 69-205, 'N', 207-564, 'L', 566-594 #label KEL

#experimental\_source brain  
REFERENCE P00157  
#authors Cram, D.S.; Barnet, L.D.; Joseph, J.T.; Harrison, L.C.  
#journal Biochem. Biophys. Res. Commun. (1991) 176:1239-1244  
#title Cloning and partial nucleotide sequence of human glutamic acid decarboxylase cDNA from brain and pancreatic islets.  
#cross-references M01D:91248209  
#accession P00157  
#molecule\_type mRNA  
#residues 218-463 #label CRI

#cross-references GB:M70434  
#experimental\_source brain  
#accession P00158

##molecule\_type mRNA  
#residues 218-234,'K',236-240,'N',242-288,'H',290-323,'L',325-329,  
#cross-references GB:M70435; NID:g182941; PID:g182942  
#experimental\_source pancreatic islet  
REFERENCE A41367  
#authors Michelsen, B.K.; Petersen, J.S.; Boel, E.; Moldrup, A.;  
#journal Proc. Natl. Acad. Sci. U.S.A. (1991) 88:8754-8758  
#title Cloning, characterization, and autoimmune recognition of rat  
islet glutamic acid decarboxylase in insulin-dependent  
diabetes mellitus.  
#cross-references MUID:92020930  
#accession B41367  
##molecule\_type mRNA  
#residues 317-482,'R',484-594 ##label MIC  
REFERENCE A36463  
#authors Persson, H.; Pelto-Huikko, M.; Metsis, M.; Soeder, O.; Brene,  
S.; Skog, S.; Hoekfelt, T.; Ritzén, E.M.  
#journal Mol. Cell. Biol. (1990) 10:4701-4711  
#title Expression of the neurotransmitter-synthesizing enzyme  
glutamic acid decarboxylase in male germ cells.  
#cross-references MUID:90355986  
#accession A36463  
##molecule\_type mRNA  
#residues 527-594 ##label PER  
#cross-references GB:M55574; NID:g182929; PIDN:AAV2938.1; PID:g182930  
REFERENCE A54778  
#authors Bu, D.F.; Tobin, A.J.  
#journal Genomics (1994) 21:222-228  
#title The exon-intron organization of the genes (GAD1 and GAD2)  
encoding two human glutamate decarboxylases (GAD-67 and  
GAD-65) suggests that they derive from a common ancestral  
GAD.  
#cross-references MUID:94375018  
#contents annotation: intron-exon organization  
COMMENT This enzyme (GAD) catalyzes the formation of an inhibitory  
neurotransmitter, gamma-aminobutyric acid, from L-glutamic acid;  
it has several isoforms, each encoded by a separate gene. GAD has  
also been implicated as an autoantigen in autoimmune disease  
stiff-man syndrome and insulin-dependent diabetes mellitus.  
GENETICS  
#gene GDB:GAD1; GAD  
#cross-references GDB:119244; OMIM:266100  
#map\_position 2q31-2q31  
CLASSIFICATION #superfamily human glutamate decarboxylase  
KEYWORDS alternative splicing; carbon-carbon lyase; carboxy-lyase;  
phosphoprotein; pyridoxal phosphate  
FEATURE 405  
#binding\_site pyridoxal phosphate (lys) (covalent)  
#status predicted  
SUMMARY #length 594 #molecular-weight 66924 #checksum 6189  
Query Match 91.2%; Score 134; DB 1; Length 594;  
Best Local Similarity 80.0%; Pred. No. 1,62e-15;  
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;  
DB 175 TLKVGRTGHPREFNQLSTG 194  
||||:||||:||||:||||:  
QY 1 TLKAIKIGHPRYFNQLSTG 20  
RESULT 11  
ENTRY JC4065 #type complete  
TITLE glutamate decarboxylase (EC 4.1.1.15) 67k chain - pig  
#formal\_name Sus scrofa domestica #common\_name domestic pig  
ORGANISM 30-Jun-1995 #sequence\_revision 14-Jul-1995 #text\_change  
DATE 22-Jun-1999  
ACCESSIONS JC4065  
REFERENCE JC4064  
#authors Suzuki, R.; Asami, N.; Amann, E.; Wagatsuna, M.  
#journal Gene (1995) 152:257-260  
#title Sequences of two porcine glutamic acid decarboxylases (65-and

67-kDa GAD)  
#cross-references MUID:95137399  
#accession JC4065  
##molecule\_type mRNA  
#residues 1-594 ##label SUZ  
#cross-references DBJ:D31849; NID:9790966; PIDN:BA06636.1;  
PID:di007208; PID:g790967  
#experimental\_source brain  
COMMENT This enzyme catalyzes the conversion of glutamic acid into  
gamma-amino butyric acid.  
CLASSIFICATION #superfamily human glutamate decarboxylase  
KEYWORDS carbon-carbon lyase; carboxy-lyase  
FEATURE 402-405  
#domain DOPA decarboxylase binding #status predicted  
SUMMARY #length 594 #molecular-weight 66894 #checksum 5491  
Query Match 91.2%; Score 134; DB 2; Length 594;  
Best Local Similarity 80.0%; Pred. No. 1,62e-15;  
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;  
DB 175 TLKVGRTGHPREFNQLSTG 194  
||||:||||:||||:||||:  
QY 1 TLKAIKIGHPRYFNQLSTG 20  
RESULT 12  
ENTRY S51775 #type complete  
TITLE glutamate decarboxylase (EC 4.1.1.15) - human  
#formal\_name Homo sapiens #common\_name man  
ORGANISM 15-Jul-1995 #sequence\_revision 21-Jul-1995 #text\_change  
DATE 22-Jun-1999  
ACCESSIONS S51775  
REFERENCE S51775  
#authors Johnstone, A.  
#submission submitted to the EMBL Data Library, May 1993  
#accession S51775  
#status preliminary  
##molecule\_type mRNA  
#residues 1-594 ##label JOH  
#cross-references EMBL:222750; NID:g298098; PIDN:CAA80435.1;  
PID:g298099  
CLASSIFICATION #superfamily human glutamate decarboxylase  
KEYWORDS carbon-carbon lyase; carboxy-lyase  
SUMMARY #length 594 #molecular-weight 66973 #checksum 6437  
Query Match 91.2%; Score 134; DB 2; Length 594;  
Best Local Similarity 80.0%; Pred. No. 1,62e-15;  
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;  
DB 175 TLKVGRTGHPREFNQLSTG 194  
||||:||||:||||:||||:  
QY 1 TLKAIKIGHPRYFNQLSTG 20  
RESULT 13  
ENTRY A46758 #type complete  
TITLE glutamate decarboxylase GAD67; L-glutamate 1-carboxy-lyase  
#formal\_name Felis silvestris catus #common\_name domestic cat  
ORGANISM 31-Dec-1993 #sequence\_revision 23-Mar-1995 #text\_change  
DATE 18-Jun-1999  
ACCESSIONS A46758  
REFERENCE A46758  
#authors Kobayashi, Y.; Kaufman, D.L.; Tobin, A.J.  
#submission submitted to GenBank, September 1989  
#accession A46758  
##molecule\_type mRNA  
#residues 1-594 ##label KOB  
#cross-references GB:M16629; NID:g163858; PIDN:AAA1430.1; PID:g163859  
REFERENCE A4671  
#authors Kobayashi, Y.; Kaufman, D.L.; Tobin, A.J.  
#journal J. Neurosci. (1987) 7:2768-2772

#title Glutamic acid decarboxylase cDNA: nucleotide sequence  
#cross-references M01D:87310623  
#accession A45671  
#molecule-type mRNA  
#residues 1-556, 'RGTRPTSGSSRRQLHSPITSSRR', ##label K02  
#note this sequence has been revised in reference A46758  
COMMENT This enzyme (GAD) catalyzes the formation of an inhibitory neurotransmitter, gamma-aminobutyric acid, from L-glutamic acid; it has several isoforms, each encoded by a separate gene.

GENETICS  
#gene GAD1  
CLASSIFICATION #superfamily human glutamate decarboxylase  
KEYWORDS #carbon-carbon lyase; carboxy-lyase; phosphoprotein; pyridoxal phosphate

FEATURE 405  
#binding-site pyridoxal phosphate (Lys) (covalent)  
#status predicted  
#length 594 #molecular-weight 66824 #checksum 5630

SUMMARY  
Query Match 91.2%; Score 134; DB 1; Length 594;  
Best Local Similarity 80.0%; Pred. No. 1.62e-15;  
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Db 175 TLKYVKTGHPHFNOJLSTG 194  
|||||:|||||:|||||  
QY 1 TLKYAIKTGHPHFNOJLSTG 20

RESULT 14  
ENTRY A30999 #type complete  
TITLE glutamate decarboxylase (EC 4.1.1.15) Cl - fruit fly  
(Drosophila melanogaster)  
ALTERNATE\_NAMES L-glutamate 1-carboxy-lyase  
ORGANISM #formal name Drosophila melanogaster  
DATE 26-Oct-1989 #sequence\_revision 23-Mar-1995 #text\_change 18-Jun-1998  
JH0192; PS0301; A30999

ACCESSIONS  
REFERENCE JH0192  
#authors Jackson, F.R.; Newby, L.M.; Kulkarni, S.J.  
#journal J. Neurochem. (1990) 54:1068-1078  
#title Drosophila GABAergic systems: sequence and expression of glutamic acid decarboxylase.  
#cross-references M01D:90155291  
#accession JH0192  
#molecule-type mRNA  
#residues 1-510 ##label JAC  
#cross-references GB:X76198; NID:g433082; PIDN:CA53791.1; PID:g433083  
#accession PS0301  
#molecule-type mRNA

COMMENT This enzyme (GAD) catalyzes the formation of an inhibitory neurotransmitter, gamma-aminobutyric acid, from L-glutamic acid; it has several isoforms, each encoded by a separate gene.

GENETICS  
#gene FlyBase:Gad1  
CLASSIFICATION #cross-references FlyBase:FBgn0004516  
KEYWORDS #superfamily human glutamate decarboxylase  
#carbon-carbon lyase; carboxy-lyase; phosphoprotein; pyridoxal phosphate

FEATURE 322  
#binding-site pyridoxal phosphate (Lys) (covalent)  
#status predicted  
#length 510 #molecular-weight 57758 #checksum 3194

SUMMARY  
Query Match 83.7%; Score 123; DB 1; Length 510;  
Best Local Similarity 75.0%; Pred. No. 6.52e-13;  
Matches 15; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Db 92 TLKYVKTGHPHFNOJLSTG 111  
|||||:|||||:|||||  
QY 1 TLKYAIKTGHPHFNOJLSTG 20

RESULT 15  
ENTRY S71489 #type complete  
TITLE sulfoalanine decarboxylase (EC 4.1.1.29) - rat  
ALTERNATE\_NAMES cysteine sulfinic acid decarboxylase  
ORGANISM #formal name Rattus norvegicus #common name Norway rat  
DATE 09-Dec-1997 #sequence\_revision 09-Dec-1997 #text\_change 22-Jun-1999  
JH1489; S78208; S55689; S55690

ACCESSIONS  
REFERENCE S71489  
#authors Raymond, I.; Sergeant, A.; Tappaz, M.  
#journal Biochim. Biophys. Acta (1996) 1307:152-156  
#title Molecular cloning and sequence analysis of the cDNA encoding rat liver cysteine sulfinic acid decarboxylase (CSD).  
#cross-references M01D:96283809  
#accession S71489  
#molecule-type mRNA  
#residues 1-493 ##label REV  
#cross-references EMBL:X94152; NID:g1263163; PIDN:CA63868.1; PID:e218415; PID:g1263164  
#experimental source liver

REFERENCE S78208  
#molecule-type protein  
#residues 9-22;106-124;467-484 ##label REM

REFERENCE S55689  
#authors Kaisaki, P.J.; Jerkins, A.A.; Goodspeed, D.C.; Steele, R.D.  
#journal Biochim. Biophys. Acta (1995) 1262:79-82  
#title Cloning and characterization of rat cysteine sulfinic acid decarboxylase.  
#cross-references M01D:95290499  
#note the author's name has been corrected in reference S60723  
#accession S55689  
#molecule-type mRNA  
#residues 1-117, 'V', 179-457, 'W', 459, 'PGFTSSDMMWPTPYWSNP', ##label KAI

#cross-references EMBL:M64755; NID:g847652; PIDN:AAC42063.1; PID:g847653

REFERENCE S55690  
#accession S55690  
#status preliminary  
#molecule-type protein  
#residues 220-230 ##label KAZ

REFERENCE S60723  
#authors Kaisaki, P.J.; Jerkins, A.A.; Goodspeed, D.C.; Steele, R.D.  
#journal Biochim. Biophys. Acta (1995) 1263:179  
#note annotation: erratum  
#note this a correction of the author's name from reference S55689  
CLASSIFICATION #superfamily human glutamate decarboxylase  
KEYWORDS #carbon-carbon lyase; carboxy-lyase; phosphoprotein; pyridoxal phosphate

FEATURE 305  
#binding-site pyridoxal phosphate (Lys) (covalent)  
#status predicted  
#length 493 #molecular-weight 55248 #checksum 7887

SUMMARY  
Query Match 73.5%; Score 108; DB 2; Length 493;  
Best Local Similarity 63.2%; Pred. No. 1.83e-09;  
Matches 12; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Db 78 IHYSVKTGHPHFNOJLSTG 96  
|||||:|||||:|||||  
QY 2 LKYAIKTGHPHFNOJLSTG 20

Search completed: Tue Mar 7 21:35:34 2000  
Job time : 9 secs.





```

DB      166 TLKYAIKTGHPRYFNOLSTG 185
      |||||||
OY      1 TLKYAIKTGHPRYFNOLSTG 20

RESULT  2
ID      DCE2_PIG      STANDARD:      PRT:      585 AA.
AC      P48321.
DT      01-FEB-1996 (Rel. 33, Created)
DT      01-FEB-1996 (Rel. 33, Last sequence update)
DT      01-FEB-1996 (Rel. 33, Last annotation update)
DE      GLUTAMATE DECARBOXYLASE, 65 KD ISOFORM (EC 4.1.1.15) (GAD-65)
DE      (65 KD GLUTAMIC ACID DECARBOXYLASE).
GN      GAD2 OR GAD65.
OS      Sus scrofa (Pig).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC      Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE-BRAIN;
RC      MEDLINE: 95137399.
KA      SUZUKI R., ASAMI N., AMANN E., WAGATSUMA M.;
RT      "Sequences of two porcine glutamic acid decarboxylases (65- and
RT      67-kDa GAD).";
RT      Gene 152:257-260(1995).
CC      -1- FUNCTION: CATALYZES THE PRODUCTION OF GABA.
CC      -1- CATALYTIC ACTIVITY: L-GLUTAMATE = 4-AMINOBUTANOATE + CO(2).
CC      -1- COFACTOR: PYRIDOXAL PHOSPHATE.
CC      -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC      -1- SIMILARITY: BELONGS TO GROUP II DECARBOXYLASES (DDC, GAD, HDC AND
CC      TYRDC).
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is in no way
CC      modified and this statement is not removed. Usage by and for commercial
CC      entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).
CC      -----
CC      EMBL: D31848; BAA06635.1; -
DR      PROSITE: PS00392; DDC_GAD_HDC_YDC: 1.
DR      PFAM: PF00282; pyridoxal_dec: 1.
KM      Neurotransmitter biosynthesis; Lyase; Decarboxylase;
KM      pyridoxal phosphate; Multigene family.
FT      BINDING: 396 396 PYRIDOXAL PHOSPHATE (POTENTIAL).
SQ      SEQUENCE 585 AA; 65388 MW; F3E9BD88 CRC32;

Query Match      100.0%; Score 147; DB 1; Length 585;
Best Local Similarity 100.0%; Pred. No. 6,54e-21;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB      166 TLKYAIKTGHPRYFNOLSTG 185
      |||||||
OY      1 TLKYAIKTGHPRYFNOLSTG 20

RESULT  3
ID      DCE2_HUMAN      STANDARD:      PRT:      585 AA.
AC      O05329;
DT      01-FEB-1996 (Rel. 33, Created)
DT      01-FEB-1996 (Rel. 33, Last sequence update)
DT      01-FEB-1996 (Rel. 33, Last annotation update)
DE      GLUTAMATE DECARBOXYLASE, 65 KD ISOFORM (EC 4.1.1.15) (GAD-65)
DE      (65 KD GLUTAMIC ACID DECARBOXYLASE).
GN      GAD2 OR GAD65.
OS      Homo sapiens (Human)
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC      Eutheria; Primates; Catarrhini; Hominoidea; Homo.
RN      [1]
RP      SEQUENCE FROM N.A.
RC      MEDLINE: 92196068.
KA      BU D.-F., ERLANDER M.G., HITZ B.C., TILLAKARATNE N.J., KAUFMAN D.L.,

```

```

RA      WAGNER-McHERSON C.B., EVANS G.A., TOBIN A.J.;
RT      "Two human glutamate decarboxylases, 65-kDa GAD and 67-kDa GAD, are
RT      each encoded by a single gene.";
RT      Proc. Natl. Acad. Sci. U.S.A. 89:2115-2119(1992).
RN      [2]
RP      SEQUENCE FROM N.A.
RC      MEDLINE: 94375018.
KA      BU D.-F., TOBIN A.J.;
RT      "The exon-intron organization of the genes (GAD1 and GAD2) encoding
RT      two human glutamate decarboxylases (GAD67 and GAD65) suggests that
RT      they derive from a common ancestral GAD.";
RT      Genomics 21:222-228(1994).
RN      [3]
RP      SEQUENCE FROM N.A.
RC      TISSUE-PANCREATIC ISLETS;
RC      MEDLINE: 92020848.
KA      KARLSEN A.E., HAGOPIAN W.A., GRUBIN C.E., DUKE S., DISTECHE C.M.,
RA      ADLER D.A., BARMETER H., MATHIEMES S., GRANT F.J., FOSTER D.,
RA      LERMARK A.;
RT      "Cloning and primary structure of a human islet isoform of glutamic
RT      acid decarboxylase from chromosome 10.";
RT      Proc. Natl. Acad. Sci. U.S.A. 88:8337-8341(1991).
RN      [4]
RP      SEQUENCE OF 6-585 FROM N.A.
RC      TISSUE-PANCREAS;
RC      MEDLINE: 93185681.
KA      MAUCH L., ABNEY C.C., BERG H., SCHERBAUM W.A., LIEBVOGEL B.,
RA      NORTHEMAN W.;
RT      "Characterization of a linear epitope within the human pancreatic
RT      64-kDa glutamic acid decarboxylase and its autoimmune recognition by
RT      sera from insulin-dependent diabetes mellitus patients.";
RT      Eur. J. Biochem. 212:597-603(1993).
CC      -1- FUNCTION: CATALYZES THE PRODUCTION OF GABA.
CC      -1- CATALYTIC ACTIVITY: L-GLUTAMATE = 4-AMINOBUTANOATE + CO(2).
CC      -1- COFACTOR: PYRIDOXAL PHOSPHATE.
CC      -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC      -1- SIMILARITY: LOCAL TO DOPA DECARBOXYLASE, AND TO PLP-TYPE HISTIDINE
CC      DECARBOXYLASE.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is in no way
CC      modified and this statement is not removed. Usage by and for commercial
CC      entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).
CC      -----
CC      EMBL: M81882; AAA62367.1; -
DR      EMBL: M74826; AAA58491.1; -
DR      EMBL: X69936; CAA49554.1; ALT_INIT.
DR      EMBL: M70435; AAA52513.1; -
DR      PIR: A41292; A41292.
DR      PIR: P00158; P00158.
DR      MIM: 138275; -
DR      PROSITE: PS00392; DDC_GAD_HDC_YDC: 1.
DR      PFAM: PF00282; pyridoxal_dec: 1.
KM      Neurotransmitter biosynthesis; Lyase; Decarboxylase;
KM      pyridoxal phosphate; Multigene family.
FT      BINDING: 396 396 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
SQ      SEQUENCE 585 AA; 65411 MW; 8AD62B62 CRC32;

Query Match      100.0%; Score 147; DB 1; Length 585;
Best Local Similarity 100.0%; Pred. No. 6,54e-21;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB      166 TLKYAIKTGHPRYFNOLSTG 185
      |||||||
OY      1 TLKYAIKTGHPRYFNOLSTG 20

RESULT  4
ID      DCE2_MOUSE      STANDARD:      PRT:      585 AA.
AC      P48320; O35519;

```

DT 01-FEB-1996 (Rel. 33, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 15-JUL-1998 (Rel. 36, Last annotation update)  
 DE GLUTAMATE DECARBOXYLASE, 65 KD ISOFORM (EC 4.1.1.15) (GAD-65)  
 GN GAD2 OR GAD65.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-C57BL/6; TISSUE-BRAIN;  
 RX MEDLINE: 94032481.  
 RA LEE D.S., TIAN J., PHAN T., KAUFMAN D.L.;  
 RT Cloning and sequence analysis of a murine cDNA encoding glutamate  
 RT decarboxylase (GAD65)."  
 RL Biochim. Biophys. Acta 1216:157-160(1993).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-C57BL/6; TISSUE-BRAIN;  
 RX MEDLINE: 97115675.  
 RA ASADA H., KAMAMURA Y., MARUYAMA K., KUWE H., DING R.G., JI F.Y.,  
 RA KANBARA N., KUZUME H., SANBO M., YAGI T., OBARA K.;  
 RT "Mice lacking the 65 kDa isoform of glutamic acid decarboxylase  
 RT (GAD65) maintain normal levels of GAD67 and GABA in their brains but  
 RT are susceptible to seizures."  
 RL Biochem. Biophys. Res. Commun. 229:891-895(1996).  
 RN [3]  
 RP SEQUENCE OF 175-379 FROM N.A.  
 RC TISSUE-BRAIN;  
 RX MEDLINE: 94062679.  
 RA FAULKNER-JONES B.E., CRAM D.S., KUN J., HARRISON L.C.;  
 RT "Localisation and quantitation of expression of two glutamate  
 RT decarboxylase genes in pancreatic beta-cells and other peripheral  
 RT tissues of mouse and rat."  
 RL Endocrinology 133:2962-2972(1993).  
 CC -1- FUNCTION: CATALYZES THE PRODUCTION OF GABA.  
 CC -1- CATALYTIC ACTIVITY: L-GLUTAMATE + 4-AMINOBUTANOATE + CO(2).  
 CC -1- COFACTOR: PYRIDOXAL PHOSPHATE.  
 CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).  
 CC -1- SIMILARITY: LOCAL TO DOPA DECARBOXYLASE, AND TO PLP-TYPE HISTIDINE  
 CC DECARBOXYLASE.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL: L16980; AAA3049.1; -  
 DR EMBL: DA2051; BAA22893.1; -  
 DR EMBL: S67454; CAB32805.1; -  
 DR MGI: 95632; GAD2.  
 DR PROSITE: PS00392; DDC\_GAD\_HDC\_YDC; 1.  
 DR PFM: PF00282; Pyridoxal\_dec; 1.  
 KW Neurotransmitter biosynthesis; Lyase; Decarboxylase;  
 KW Pyridoxal phosphate; Multigene family.  
 FT BINDING 396  
 FT CONFLICT 259 396 PYRIDOXAL PHOSPHATE (POTENTIAL).  
 FT CONFLICT 319 396 E -> S (IN REF. 2).  
 FT CONFLICT 325 325 I -> S (IN REF. 3).  
 FT CONFLICT 499 499 K -> E (IN REF. 2).  
 FT CONFLICT 499 499 P -> S (IN REF. 2).  
 SQ SEQUENCE 585 AA; 65224 MW; 9BESC088 CRC32;

Query Match 100.0%; Score 147; DB 1; Length 585;  
 Best Local Similarity 100.0%; Pred. No. 6,54e-21;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 166 TLKAITGHPREFNOLSTG 185  
 |||||  
 QY 1 TLKAITGHPREFNOLSTG 20

RESULT 5  
 ID DECI\_MOUSE STANDARD; PRT; 593 AA.  
 AC P48318;  
 DT 01-FEB-1996 (Rel. 33, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DE GLUTAMATE DECARBOXYLASE, 67 KD ISOFORM (EC 4.1.1.15) (GAD-67)  
 GN GAD1 OR GAD67.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-BRAIN;  
 RX KATAROVA Z., SZABO G., MUGNANI E., GREENSPAN R.;  
 RT "Molecular identification of the 62 kd form of glutamic acid  
 RT decarboxylase from the mouse."  
 RL Eur. J. Neurosci. 2:190-202(1990).  
 RN [2]  
 RP SEQUENCE OF 198-403 FROM N.A.  
 RC TISSUE-BRAIN;  
 RX MEDLINE: 94062679.  
 RA FAULKNER-JONES B.E., CRAM D.S., KUN J., HARRISON L.C.;  
 RT "Localisation and quantitation of expression of two glutamate  
 RT decarboxylase genes in pancreatic beta-cells and other peripheral  
 RT tissues of mouse and rat."  
 RL Endocrinology 133:2962-2972(1993).  
 CC -1- FUNCTION: CATALYZES THE PRODUCTION OF GABA.  
 CC -1- CATALYTIC ACTIVITY: L-GLUTAMATE + 4-AMINOBUTANOATE + CO(2).  
 CC -1- COFACTOR: PYRIDOXAL PHOSPHATE.  
 CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO GROUP II DECARBOXYLASES (DDC, GAD, HDC AND  
 CC TYRDC).  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL: Z49976; CAA3027.1; -  
 DR EMBL: S67453; CAB32805.1; -  
 DR MGI: 95632; GAD1.  
 DR PROSITE: PS00392; DDC\_GAD\_HDC\_YDC; 1.  
 DR PFM: PF00282; Pyridoxal\_dec; 1.  
 KW Neurotransmitter biosynthesis; Lyase; Decarboxylase;  
 KW Pyridoxal phosphate; Multigene family.  
 FT BINDING 404  
 FT CONFLICT 234 404 PYRIDOXAL PHOSPHATE (POTENTIAL).  
 FT CONFLICT 258 258 E -> K (IN REF. 2).  
 FT CONFLICT 360 360 S -> T (IN REF. 1).  
 FT CONFLICT 360 360 D -> S (IN REF. 1).  
 SQ SEQUENCE 593 AA; 66584 MW; 63BC57AA CRC32;

Query Match 91.2%; Score 134; DB 1; Length 593;  
 Best Local Similarity 80.0%; Pred. No. 1.91e-17;  
 Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Db 174 TLKGYRGHPREFNOLSTG 193  
 |||||  
 QY 1 TLKGYRGHPREFNOLSTG 20

RESULT 6  
 ID DECI\_RAT STANDARD; PRT; 593 AA.  
 AC P18088;  
 DT 01-NOV-1990 (Rel. 16, Created)  
 DT 01-NOV-1990 (Rel. 16, Last sequence update)  
 DT 01-FEB-1996 (Rel. 33, Last annotation update)

```

DE GLUTAMATE DECARBOXYLASE, 67 KD ISOFORM (EC 4.1.1.15) (GAD-67)
DE (67 KD GLUTAMIC ACID DECARBOXYLASE).
GN GAD1 OR GAD67.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 91014554.
RA WYORSKI R.J., BOND R.W., GOTTLIEB D.I.;
RT "Characterization of a cDNA coding for rat glutamic acid
RT decarboxylase."
RL Brain Res. Mol. Brain Res. 8:193-198(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE: 90132703.
RA JULIEN J.F., SAMAMA P., MALLET J.;
RT "Rat brain glutamic acid decarboxylase sequence deduced from a cloned
RT cDNA."
RL J. Neurochem. 54:703-705(1990).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE: 92020930.
RA MICHELSEN B.K., PETERSEN J.S., BOEL E., MOLDROP A., DYBERG T.,
RA MADSEN O.D.;
RT "Cloning, characterization, and autoimmune recognition of rat islet
RT glutamic acid decarboxylase in insulin-dependent diabetes mellitus."
RL Proc. Natl. Acad. Sci. U.S.A. 88:8754-8758(1991).
CC -1- FUNCTION: CATALYZES THE PRODUCTION OF GABA.
CC -1- CATALYTIC ACTIVITY: L-GLUTAMATE = 4-AMINOBUTANOATE + CO(2).
CC -1- COFACTOR: PYRIDOXAL PHOSPHATE.
CC -1- SUBUNIT: HOMODIMER.
CC -1- SIMILARITY: BELONGS TO GROUP II DECARBOXYLASES (DDC, GAD, HDC AND
CC TYRDC).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: M34445; AAC42037.1; -
DR EMBL: X57572; CAA40800.1; -
DR EMBL: X57573; CAA40801.1; -
DR EMBL: M76177; AAA41184.1; -
DR PIR: A41367; A41367.
DR PIR: A43756; A43756.
DR PROSITE: PS00392; DDC_GAD_HDC_YDC.1.
DR PFAM: PF00282; pyridoxal_dec.1.
KW Neurotransmitter biosynthesis; Lyase; Decarboxylase;
KW Pyridoxal phosphate; Multigene family.
FT BINDING 404 404 PYRIDOXAL PHOSPHATE (POTENTIAL).
FT CONFLICT 103 103 L -> V (IN REF. 2).
FT CONFLICT 284 284 E -> S (IN REF. 2).
FT CONFLICT 287 288 EH -> AD (IN REF. 2).
FT CONFLICT 344 345 AG -> EA (IN REF. 2).
FT CONFLICT 347 347 T -> I (IN REF. 2).
FT CONFLICT 352 353 FD -> LE (IN REF. 2).
FT CONFLICT 380 380 L -> R (IN REF. 2).
SQ SEQUENCE 593 AA; 66640 MW; 5A0B67C0 CRC32;

```

Query Match 91.2%; Score 134; DB 1; Length 593;  
 Best Local Similarity 80.0%; Pred. No. 1,91e-17;  
 Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Db 174 TLKYGVRGHPFFNOLSTG 193  
 |||||:|||||:|||||  
 1 TLKVAIKTGHPFFNOLSTG 20

RESULT 7

```

ID DCE1_PIG STANDARD; PRT; 594 AA.
AC P48319.
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE GLUTAMATE DECARBOXYLASE, 67 KD ISOFORM (EC 4.1.1.15) (GAD-67)
DE (67 KD GLUTAMIC ACID DECARBOXYLASE).
GN GAD1 OR GAD67.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN.
RX MEDLINE: 95137399.
RA SUZUKI R., ASAMI N., WAGATSUMA M.;
RT "Sequences of two porcine glutamic acid decarboxylases (65- and
RT 67-kDa GAD)."
RL Gene 152:257-260(1995)
CC -1- FUNCTION: CATALYZES THE PRODUCTION OF GABA.
CC -1- CATALYTIC ACTIVITY: L-GLUTAMATE = 4-AMINOBUTANOATE + CO(2).
CC -1- COFACTOR: PYRIDOXAL PHOSPHATE.
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO GROUP II DECARBOXYLASES (DDC, GAD, HDC AND
CC TYRDC).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: D31849; BAA06636.1; -
DR PROSITE: PS00392; DDC_GAD_HDC_YDC.1.
DR PFAM: PF00282; pyridoxal_dec.1.
KW Neurotransmitter biosynthesis; Lyase; Decarboxylase;
KW Pyridoxal phosphate; Multigene family.
FT BINDING 405 405 PYRIDOXAL PHOSPHATE (POTENTIAL).
SQ SEQUENCE 594 AA; 66894 MW; 69D6C79C CRC32;

```

Query Match 91.2%; Score 134; DB 1; Length 594;  
 Best Local Similarity 80.0%; Pred. No. 1,91e-17;  
 Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Db 175 TLKYGVRGHPFFNOLSTG 194  
 |||||:|||||:|||||  
 1 TLKVAIKTGHPFFNOLSTG 20

RESULT 8  
 ID DCE1\_HUMAN STANDARD; PRT; 594 AA.  
 AC O98259.  
 DT 01-FEB-1996 (Rel. 33, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 01-OCT-1996 (Rel. 34, Last annotation update)  
 DE GLUTAMATE DECARBOXYLASE, 67 KD ISOFORM (EC 4.1.1.15) (GAD-67)  
 DE (67 KD GLUTAMIC ACID DECARBOXYLASE).  
 GN GAD1 OR GAD.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 OC Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-BRAIN.  
 RX MEDLINE: 92196068.  
 RA BU D.-F., ERLANDER M.G., HITZ B.C., TILLARATINE N.J., KAUFMAN D.L.,  
 RA WAGNER-MCPHERSON C.B., EVANS G.A., TOBIN A.J.;  
 RT "Two human glutamate decarboxylases, 65-kDa GAD and 67-kDa GAD, are  
 RT each encoded by a single gene."  
 RL Proc. Natl. Acad. Sci. U.S.A. 89:2115-2119(1992).  
 RN [2]

RP SEQUENCE FROM N.A.  
 RX MEDLINE: 94375018.  
 RA BU D.-F., TOBIN A.J.:  
 RT "The exon-intron organization of the genes (GAD1 and GAD2) encoding  
 RT two human glutamate decarboxylases (GAD67 and GAD65) suggests that  
 RT they derive from a common ancestral GAD."  
 RL Genomics 21:222-228(1994).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-BRAIN;  
 RX MEDLINE: 93080286.  
 RA KELLY C.D., EDWARDS Y., JOHNSTONE A.P., HARFST E., NOGRADI A.,  
 RA NUSSEY S.S., POVEY S., CARTER N.D.:  
 RT "Nucleotide sequence and chromosomal assignment of a cDNA encoding  
 RT the large isoform of human glutamate decarboxylase."  
 RL Ann. Hum. Genet. 56:255-265(1992).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE: 93282844.  
 RA YAMASHITA K., GRAM D.S., HARRISON L.C.:  
 RT "Molecular cloning of full-length glutamic acid decarboxylase 67 from  
 RT human pancreas and islets."  
 RL Biochem. Biophys. Res. Commun. 192:1347-1352(1993).  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-PANCREATIC ISLETS;  
 RX MEDLINE: 93282845.  
 RA KAWASAKI E., MORIUCHI R., WATANABE M., SATOH K., BRUNICARDI F.C.,  
 RA WATT P.C., YAMAGUCHI T., MULLEN Y., AKAZAWA S., MIYAMOTO T.:  
 RT "Cloning and expression of large isoform of glutamic acid  
 RT decarboxylase from human pancreatic islet."  
 RL Biochem. Biophys. Res. Commun. 192:1353-1359(1993).  
 RN [6]  
 RP SEQUENCE FROM N.A.  
 RA GIORA R., PEAKMAN M., VERGANI D., TRUCCO M.:  
 RL Submitted (MAR-1992) to the EMBL/GenBank/DBJ databases.  
 RN [7]  
 RP SEQUENCE OF 218-397 FROM N.A.  
 RC TISSUE-BRAIN;  
 RX MEDLINE: 91248209.  
 RA GRAM D.S., BARNETT L.D., JOSEPH J.L., HARRISON L.C.:  
 RT "Cloning and partial nucleotide sequence of human glutamic acid  
 RT decarboxylase cDNA from brain and pancreatic islets."  
 RL Biochem. Biophys. Res. Commun. 176:1239-1244(1991).  
 RN [8]  
 RP SEQUENCE OF 527-594 FROM N.A.  
 RC TISSUE-TESTIS;  
 RX MEDLINE: 90355986.  
 RA PERSSON H., PELTO-HUIKKO M., METSIS M., SOEDER O., BRENE S.,  
 RA SKOG S., HOKKFELT T., RITZEN E.M.:  
 RT "Expression of the neurotransmitter-synthesizing enzyme glutamic acid  
 RT decarboxylase in male germ cells."  
 RL Mol. Cell. Biol. 10:4701-4711(1990).  
 CC -|- FUNCTION: CATALYZES THE PRODUCTION OF GABA.  
 CC -|- CATALYTIC ACTIVITY: L-GLUTAMATE = 4-AMINOBUTANOATE + CO(2).  
 CC -|- COFACTOR: PYRIDOXAL PHOSPHATE.  
 CC -|- SUBUNIT: HOMODIMER.  
 CC -|- SIMILARITY: BELONGS TO GROUP II DECARBOXYLASES (DDC, GAD, HDC AND  
 CC TYRDC).  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 CC EMBL: M81883; AAA62368.1; -  
 CC EMBL: L16888; AAB59427.1; -  
 CC EMBL: 222750; CAA80435.1; -  
 CC EMBL: S61897; AAB26937.1; -  
 CC EMBL: S61898; AAB26938.1; -

DR EMBL: M86522; AAA35900.1; -  
 DR EMBL: M70434; AAA52512.1; -  
 DR EMBL: M55574; AAA72938.1; -  
 DR EMBL: A28074; CAA01913.1; -  
 DR PIR: P00157; P00157.  
 DR MIM: 266100; -  
 DR PROSITE: PS00392; DDC\_GAD\_HDC\_YDC; 1.  
 DR PIRAM: PF00282; pyridoxal\_dec; 1.  
 KW Neurotransmitter biosynthesis; Lyase; Decarboxylase;  
 KW Pyridoxal phosphate; Multigene family.  
 FT BINDING 405 405  
 FT CONFLICT 9 9  
 FT CONFLICT 16 17  
 FT CONFLICT 17 17  
 FT CONFLICT 18 18  
 FT CONFLICT 31 31  
 FT CONFLICT 68 68  
 FT CONFLICT 116 116  
 FT CONFLICT 136 136  
 FT CONFLICT 140 140  
 FT CONFLICT 142 142  
 FT CONFLICT 155 155  
 FT CONFLICT 206 206  
 FT CONFLICT 302 302  
 FT CONFLICT 436 436  
 FT CONFLICT 512 512  
 FT CONFLICT 477 477  
 FT CONFLICT 492 492  
 FT CONFLICT 565 565  
 SQ SEQUENCE 594 AA; 66896 MM; 94733552 CAC32;  
 Query Match 91.2%; Score 134; DB 1; Length 594;  
 Best Local Similarity 80.0%; Pred. No. 1.91e-17;  
 Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;  
 Db 175 TLKRGVTRGHPREFNOUSTG 194  
 QY 1 TLKRAIKRGHPREFNOUSTG 20  
 RESULT 9  
 ID DCEL FELCA STANDARD; PRT; 594 AA.  
 AC P14748;  
 DT 01-APR-1990 (Rel. 14, Created)  
 DT 01-OCT-1993 (Rel. 27, Last sequence update)  
 DT 01-FEB-1996 (Rel. 33, Last annotation update)  
 DE GLUTAMATE DECARBOXYLASE, 67 KD ISOFORM (EC 4.1.1.15) (GAD-67)  
 DE (67 KD GLUTAMIC ACID DECARBOXYLASE).  
 GN GAD1 OR GAD67.  
 OS Felis silvestris catus (Cat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 OC Eutheria; Carnivora; Fissipedia; Felidae; Felis.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-OCIPITAL CORTEX;  
 RX MEDLINE: 87310623.  
 RA KOBAYASHI Y., KAUFMAN D.L., TOBIN A.J.:  
 RT "Glutamic acid decarboxylase cDNA: nucleotide sequence encoding an  
 RT enzymatically active fusion protein."  
 RL J. Neurosci. 7:2768-2772(1987).  
 CC -|- FUNCTION: CATALYZES THE PRODUCTION OF GABA.  
 CC -|- CATALYTIC ACTIVITY: L-GLUTAMATE = 4-AMINOBUTANOATE + CO(2).  
 CC -|- COFACTOR: PYRIDOXAL PHOSPHATE.  
 CC -|- SUBUNIT: HOMODIMER.  
 CC -|- SIMILARITY: BELONGS TO GROUP II DECARBOXYLASES (DDC, GAD, HDC AND  
 CC TYRDC).  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>

```

CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: M18629; AAAS1430.1; -
DR PIR: A45671; A45671.
DR PIR: A46758; A46758.
DR PROSITE: PS00392; DDC_GAD_HDC_YDC; 1.
DR PFAM: PF00282; pyridoxal_gdc; 1.
DR Neurotransmitter biosynthesis; Lyase; Decarboxylase;
KW pyridoxal phosphate; Multigene family.
FT BINDING 405
SQ SEQUENCE 594 AA; 66824 MW; 3EC20778 CRC32;

Query Match
Best Local Similarity 80.0%; Score 134; DB 1; Length 594;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Db 175 TLKYGVKTHGHPHFNLSTG 194
1 TLKYAIKTHGHPHFNLSTG 20

RESULT 10
AC P20228; STANDARD; PRT; 510 AA.
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE GLUTAMATE DECARBOXYLASE (EC 4.1.1.15) (GAD).
GN GAD OR GLB.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 90155291.
RA JACKSON F.R., NEWBY L.M., KUKARANI S.J.;
RA "Drosophila GABAergic systems: sequence and expression of glutamic
RT acid decarboxylase."
RL J. Neurochem. 54:1068-1078(1990).
CC -1- FUNCTION: CATALYZES THE PRODUCTION OF GABA.
CC -1- CATALYTIC ACTIVITY: L-GLUTAMATE = 4-AMINOBUTANOATE + CO(2).
CC -1- COFACTOR: PYRIDOXAL PHOSPHATE.
CC -1- SUBUNIT: HOMODIMER.
CC -1- SIMILARITY: BELONGS TO GROUP II DECARBOXYLASES (DDC, GAD, HDC AND
CC TYDC).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X76198; CAAS3791.1; -
DR PIR: A30999; A30999.
DR PIR: JH0192; JH0192.
DR FLXBASE: FBgn0004516; Gcd1.
DR PROSITE: PS00392; DDC_GAD_HDC_YDC; 1.
DR PFAM: PF00282; pyridoxal_gdc; 1.
DR Neurotransmitter biosynthesis; Lyase; Decarboxylase;
KW pyridoxal phosphate.
FT BINDING 322
SQ SEQUENCE 510 AA; 57758 MW; 97C7A8F1 CRC32;

Query Match
Best Local Similarity 83.7%; Score 123; DB 1; Length 510;
Matches 15; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Db 92 TLKYGVKTHGHPHFNLSTG 111
1 TLKYAIKTHGHPHFNLSTG 20

```

```

RESULT 11
ID YG10_ECOLI STANDARD; PRT; 413 AA.
AC Q46861.
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE HYPOTHEETICAL 46.9 KD PROTEIN IN METC-SOFT INTERGENIC REGION.
GN YG10.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-K12 / MG1655;
RX MEDLINE: 97426617.
RA BLATTNER F.R., PLUNKETT G. III, BLOCH C.A., PERNA N.T., BURLAND V.,
RA RILEY M., COLLADO-VIDES J., GLASNER F.D., RODE C.K., MAYHEW G.F.,
RA GREGOR J., DAVIS N.W., KIRKPATRICK H.A., GOEDEN W.A., ROSE D.J.,
RA MAU B., SHAO Y.;
RT "The complete genome sequence of Escherichia coli K-12."
RL Science 277:1453-1474(1997).
CC -1- SIMILARITY: TO THE C-TERMINAL OF M.JANASCHII M1155, THE N-
CC TERMINAL PART OF M1555 IS COLINEAR TO E.COLI YG10. ALSO SOME
CC SIMILARITY TO FAMILY UPF0004.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U28377; AAA69183.1; -
DR EMBL: AE000383; AAC76051.1; -
DR ECOGENE: EG19019; YG10.
KW Hypothetical protein.
SQ SEQUENCE 413 AA; 46943 MW; 8E9159B5 CRC32;

Query Match
Best Local Similarity 46.9%; Score 69; DB 1; Length 413;
Matches 7; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

Db 170 VRYDAVEDPRYKELAT 187
2 LKYAIKTHGHPHFNLST 19

RESULT 12
AC P31301; STANDARD; PRT; 391 AA.
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE DIHYDROROTAASE (EC 3.5.2.3) (DHORASE).
GN PYR3.
OS Ustilago maydis (Smut fungus).
OC Eukaryota; Fungi; Basidiomycota; Ustilaginomycetes;
OC Ustilaginomycetidae; Ustilaginales; Ustilaginaceae; Ustilago.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-521;
RX MEDLINE: 92354940.
RA SPANOS A., KANUGA N., HOLDEN D.W., BANKS G.R.;
RT "The Ustilago maydis pyr3 gene: sequence and transcriptional
RT analysis."
RL Gene 117:73-79(1992).
CC -1- CATALYTIC ACTIVITY: DIHYDROROTAATE + H(2)O = N-CARBAMOYL-
CC L-ASPARATE.
CC -1- COFACTOR: ZINC.
CC -1- PATHWAY: THIRD STEP IN PYRIMIDINE BIOSYNTHESIS.

```



Query Match 44.2% Score 65; DB 1; Length 897;  
 Best Local Similarity 50.0%; Pred. No. 4.02e-01;  
 Matches 8; Conservative 4; Mismatches 4; Indels 0; Gaps 0;  
 DB 484 KYLXSGLOKYNOLG 499  
 QY 3 KYAKTGHPRYFNLS 18

RESULT 15  
 ID YEBA\_HAEIN STANDARD; PRT; 475 AA.  
 AC P44693;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 01-NOV-1995 (Rel. 32, Last annotation update)  
 DE HYPOTHETICAL PROTEIN HI0409.  
 GN HI0409.  
 OS Haemophilus influenzae.  
 OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;  
 OC Haemophilus.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-RD / KW20;  
 RX MEDLINE; 95350630.  
 RA FLEISCHMANN R.D., ADAMS M.D., WHITE O., CLAYTON R.A., KIRKNESS E.F.,  
 KERLAVAGE A.R., BULT C.J., TOMB J.-F., DOUGHERTY B.A., MERRICK J.M.,  
 MCKENNEY K., SUTTON G., FITZHUGH W., FIELDS C.A., GOCAYNE J.D.,  
 SCOTT J.D., SHIRLEY R., LIU L.-I., GLODER A., KELLEY J.M.,  
 WEIDMAN J.F., PHILLIPS C.A., SPRIGGS T., HEDBLUM E., COTTON M.D.,  
 RA UTTERBACK T.R., HANNA M.C., NGUYEN D.T., SAUDEK D.M., BRANDON R.C.,  
 RA FINE L.D., FRITCHMAN J.L., FUHRMANN J.L., GEOGHAGEN N.S.M.,  
 RA GNEHM C.L., MCDONALD L.A., SMALL K.V., FRASER C.M., SMITH H.O.,  
 RA VENTER J.C.,  
 RT "Whole-genome random sequencing and assembly of Haemophilus  
 influenzae Rd.";  
 RL Science 269:496-512(1995).  
 CC -!- FUNCTION: COULD BE INVOLVED IN CELL WALL DEGRADATION OR  
 FORMATION (BY SIMILARITY).  
 CC -!- SIMILARITY: STRONG, TO E.COLI YEBA.  
 CC -!- SIMILARITY: TO STAPHYLOCOCCUS LYSOSTAPHIN.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL: U3724; AAC22068.1; -  
 DR TIGR: HI0409; -  
 DR PFIAM: PF01551; Peptidase\_M37; 1.  
 DR Hypothetical protein; Cell wall.  
 KW SEQUENCE 475 AA; 53255 MW; 8C160515 CRC32;

Query Match 43.5% Score 64; DB 1; Length 475;  
 Best Local Similarity 46.2%; Pred. No. 6.27e-01;  
 Matches 6; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

DB 297 YAVOANGRYNO 309  
 QY 4 YAIKTGHPRYFNQ 16

Search completed: Tue Mar 7 21:30:35 2000  
 Job time : 6 secs.





```

RA WABERG F.;
RT "Characterization of glutamate decarboxylase in chicken.";
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
CC -I- COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).
CC -I- SIMILARITY: BELONGS TO GROUP II DECARBOXYLASES (DDC, GAD, HDC AND TYDCC).
CC EMBL: AF030355; AAD01902.1; -.
DR PROSITE: PS00392; DDC_GAD_HDC_YDC; 1.
KM Lyase; Decarboxylase; Pyridoxal phosphate.
SQ SEQUENCE 590 AA; 66710 MW; 80B65DFF CRC32;

Query Match 91.2%; Score 134; DB 13; Length 590;
Best Local Similarity 80.0%; Pred. No. 6,34e-18;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Db 171 TLKYGVRGHPREFNOLSTG 190
||||:||||:||||:|
QY 1 TLKYAIKTGHPREFNOLSTG 20

RESULT 3
ID 008685 PRELIMINARY; PRT; 593 AA.
AC 008685;
DT 01-JUL-1997 (TREMBLrel. 04, Created)
DI 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
DE 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
DE 67KD GLUTAMIC ACID DECARBOXYLASE.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/C.
RA AUST G., STEINBRENNER H., THAMM B., ROST A.K., SEISSLER J.;
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
CC -I- COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).
CC -I- SIMILARITY: BELONGS TO GROUP II DECARBOXYLASES (DDC, GAD, HDC AND TYDCC).
CC EMBL: Y12557; CAN72934.1; -.
DR PROSITE: PS00392; DDC_GAD_HDC_YDC; 1.
DR PFM: PF00282; Pyridoxal_dec; 1.
KM Lyase; Decarboxylase; Pyridoxal phosphate.
SQ SEQUENCE 593 AA; 66648 MW; BAFE92E0 CRC32;

Query Match 91.2%; Score 134; DB 11; Length 593;
Best Local Similarity 80.0%; Pred. No. 6,34e-18;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Db 174 TLKYGVRGHPREFNOLSTG 193
||||:||||:||||:|
QY 1 TLKYAIKTGHPREFNOLSTG 20

RESULT 4
ID 044102 PRELIMINARY; PRT; 370 AA.
AC 044102;
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DI 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DE 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
DE GLUTAMIC ACID DECARBOXYLASE (FRAGMENT).
GN GAD1.
OS Drosophila pseudoobscura (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
RN [1]
RP SEQUENCE FROM N.A.
RC ZENG L.-W., COMERON J.M., CHEN B., KREITMAN M.;
RL Genetica 0:0-0(1997).
DR EMBL: AF025807; AAB87892.1; -.
DR HSSP: P06543; 100C.
DR FLYBASE: FBgn0023295; Dpse\Gad1.
DR PFM: PF00282; pyridoxal_dec; 2.

```

```

FT NON_TER 1 1
FT NON_TER 370 370
SQ SEQUENCE 370 AA; 41887 MW; A1EB456F CRC32;

Query Match 83.7%; Score 123; DB 5; Length 370;
Best Local Similarity 75.0%; Pred. No. 5,61e-15;
Matches 15; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Db 12 TLKYVKTGHPREFNOLSTG 31
||||:||||:||||:|
QY 1 TLKYAIKTGHPREFNOLSTG 20

RESULT 5
ID 044103 PRELIMINARY; PRT; 370 AA.
AC 044103;
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DI 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DE 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
DE GLUTAMIC ACID DECARBOXYLASE (FRAGMENT).
GN GAD1.
OS Drosophila subobscura (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
RN [1]
RP SEQUENCE FROM N.A.
RC ZENG L.-W., COMERON J.M., CHEN B., KREITMAN M.;
RL Genetica 0:0-0(1997).
DR EMBL: AF025808; AAB87893.1; -.
DR HSSP: P06543; 100C.
DR FLYBASE: FBgn0023244; Dsub\Gad1.
DR PFM: PF00282; pyridoxal_dec; 2.
FT NON_TER 1 1
FT NON_TER 370 370
SQ SEQUENCE 370 AA; 41923 MW; D75BDC49 CRC32;

Query Match 83.7%; Score 123; DB 5; Length 370;
Best Local Similarity 75.0%; Pred. No. 5,61e-15;
Matches 15; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Db 12 TLKYVKTGHPREFNOLSTG 31
||||:||||:||||:|
QY 1 TLKYAIKTGHPREFNOLSTG 20

RESULT 6
ID 09Y602 PRELIMINARY; PRT; 267 AA.
AC 09Y602;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DI 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DE 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
DE CYSTEINE SULFINIC ACID DECARBOXYLASE-RELATED PROTEIN 1.
GN CSAD.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RC PRITCHARD J.E., RAMSDEN D.B.;
RT "Human cysteine sulfinic acid decarboxylase (CSAD)-related mRNA, 1.";
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF116545; AAD2543.1; -.
SQ SEQUENCE 267 AA; 30264 MW; A3475A7D CRC32;

Query Match 76.9%; Score 113; DB 4; Length 267;
Best Local Similarity 63.2%; Pred. No. 2,33e-12;
Matches 12; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Db 78 IRYSVKTGHPREFNOLSTG 96
||||:||||:||||:|
QY 2 LKYAIKTGHPREFNOLSTG 20

```

RESULT	7			
ID	09Y600	PRELIMINARY:	PRT:	493 AA.
AC	Q9Y600.			
DT	01-NOV-1999	(TREMBLrel. 12,		
DT	01-NOV-1999	(TREMBLrel. 12,		
DT	01-NOV-1999	(TREMBLrel. 12,		
DE	CYS-NE SULFINIC ACID DECARBOXYLASE-RELATED PROTEIN 3.			
GN	CSAD.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;			
NN	Mammalia; Primates; Catarrhini; Homidae; Homo.			
LN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE-BRAIN:			
RA	FITCHARD J.E., RAMSDEN D.B.;			
RT	"Human cysteine sulfinic acid decarboxylase (CSAD)-related mRNA, 3.";			
RL	Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.			
DR	EMBL: AF116547; AAD32545.1; "			
SO	SEQUENCE 493 AA; 54951 MW; F4852742 CRC32;			
Query Match	76.9%;	Score 113;	DB 4;	Length 493;
Best Local Similarity	63.2%;	Pred. No. 2,336-12;		
Matches 12;	Conservative	6;	Mismatches 1;	Indels 0;
Gaps				0;
Db	78 IRISVTGTHPRFFNOLFGS 96			
	:::::     ::   :: :			
OY	2 LKVAIKTGHPRFFNOLSTG 20			

RESULT	8	PRELIMINARY;	PRT;	78 AA.
ID	P70713			
AC	P70713.			
DT	01-FEB-1997 (TREMBLrel. 02, Created)			
DT	01-FEB-1997 (TREMBLrel. 02, Last sequence update)			
DT	01-MAY-1999 (TREMBLrel. 10, Last annotation update)			
DE	CYSINE SULFINATE DECARBOXYLASE (EC 4.1.1.29)			
DE	(SULFINOALANINE DECARBOXYLASE) (CYSINE-SULFINATE DECARBOXYLASE)			
DE	(FRAGMENT).			
OS	Rattus norvegicus (Rat).			
OC	Eumetazoa; Metazoa; Chordata; Craniota; Vertebrata; Mammalia;			
OC	Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			
RN	(1)			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-SPRAGUE-DAWLEY; TISSUE=LIVER;			
RA	KRATSKIN I. L., YU X., SMUTZER G., DOTY R. L.;			
RL	Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.			
CC	-1- CATALYTIC ACTIVITY: 3-SULFINO-L-ALANINE = HYPOTAURINE + CO(2).			
CC	-1- COPACTOR: PYRIDOXAL-PHOSPHATE.			
DR	EMBL; U74492; AAB1832.1; -			
DR	PFAM; PF00282; Pyridoxal_dec; 1.			
KW	Lysase.			
FT	NON_TER	1	1	
FT	NON_TER	78	78	
SO	SEQUENCE	78 AA;	9134 MW;	F4808DJF CRC32;
	Query Match	73.5%;	Score 108;	DB 11; Length 78;
	Best Local Similarity	63.2%;	Pred. No. 4,48e-11;	
	Matches 12; Conservative	5;	Mismatches 2;	Indels 0; Gaps 0
DB	37 IH5VKTGHPREFNOLFSG 55			
	: :: :: :: :: :: ::			
Qy	2 LKVAIKTGHPRFNOLSTG 20			
RESULT	9	PRELIMINARY;	PRT;	478 AA.
ID	O64577			
AC	O64577.			
DT	01-NOV-1996 (TREMBLrel. 01, Created)			
DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)			
DT	01-NOV-1999 (TREMBLrel. 12, Last annotation update)			
DE	CYSINE SULFINIC ACID DECARBOXYLASE (EC 4.1.1.29)			

```

DE (SULFINOALANINE DECARBOXYLASE) (CYSTEINE-SULFINATE DECARBOXYLASE).
OS
OC Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN
  (1)
RP SEQUENCE FROM N.A.
RC STRAIN-SPRAGUE-DAWLEY;
RC MEDLINE; 95290489.
RA KATSAVIA P.J., JERKINS A.A., GOODSPEED D.C., STEELE R.D.;
RT "Cloning and characterization of rat cysteine sulfinic acid
RT decarboxylase."
RL Biochim. Biophys. Acta 1262:79-82(1995).
CC -I- CATALYTIC ACTIVITY: 3-SULFINO-L-ALANINE = HYDROTURINE + CO(2).
CC -I- COFACTOR: PYRIDOXAL-PHOSPHATE.
CC -I- COFACTOR: PYRIDOXAL-PHOSPHATE. (BY SIMILARITY).
CC -I- SIMILARITY: BELONGS TO GROUP II DECARBOXYLASES (DDC, GAD, HDC AND
CC TYRDC).
DR EMBL; M64755; AAC42063.1; -.
DR PROSITE; PS00392; DDC_GAD_HDC_YDC; 1.
DR PFAM; PF00282; pyridoxal_dec; 1.
KW Lyase; Decarboxylase; Pyridoxal phosphate.
SQ SEQUENCE 478 AA; 53725 MW; 4CAC0093 CRC32;

Query Match 73.5% Score 108; DB 11; Length 478;
Best Local Similarity 63.2%; Pred. No. 4,48e-11;
Matches 12; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

```

RESULT	11	PRELIMINARY:	PRT:	493 AA.
ID	064611			
AC	064611:			
DT	01-NOV-1996 (TrEMBLrel. 01, Created)			
DT	01-NOV-1996 (TrEMBLrel. 01, Last sequence update)			
DT	01-NOV-1999 (TrEMBLrel. 12, Last annotation update)			
DE	CYSTEINE SULFINATE DECARBOXYLASE (EC 4.1.1.29)			
DE	(SULFINOALANINE DECARBOXYLASE) (CYSTEINE-SULFINATE DECARBOXYLASE).			
GN	CSD.			
OS	Rattus norvegicus (Rat).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;			
OC	Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE; 96283809.			
RA	REYMOND I., SERGEANT A., TAPPAZ M.;			
RT	"Molecular cloning and sequence analysis of the cDNA encoding rat			
RT	liver cysteine sulfinate decarboxylase (CSD)."			
RL	Biochim. Biophys. Acta 1307:152-156(1995).			
CC	-I- COPACATOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).			
CC	-I- SIMILARITY: BELONGS TO GROUP II DECARBOXYLASES (DDC, GAD, HDC AND			
CC	TYRDC).			
DR	EMBL; X94152; CAA63868.1; "			
DR	PROSITE; PS00392; DDC_GAD_HDC_YDC; 1.			
DR	PFAM; PF00283; pyridoxal_dec_1			
KM	lyase; Decarboxylase; Pyridoxal phosphate.			
SO	SEQUENCE 493 AA; 55248 MW; D7A6BD9A CRC32;			
Query Match		73.5%;	Score 108;	DB 11; Length 493;
Best Local Similarity		63.2%;	Pred. No. 4,48e-11;	
Matches 12; Conservative		5;	Mismatches 2;	Indels 0; Gaps 0;
DB	78	IHSYKVTGHPREFNOLFSG 96		
	:	: : : : : : : : : : : : : :		
QY	2	LKVAIKTGHPRYFNLSTYG 20		
RESULT	11	PRELIMINARY:	PRT:	508 AA.
ID	09XTP4			
AC	09XTP4:			
DT	01-NOV-1999 (TrEMBLrel. 12, Created)			

```
DI 01-NOV-1999 (TEMBLrel. 12, last sequence update)
DI 01-NOV-1999 (TEMBLrel. 12, last annotation update)
DE GLUTAMIC ACID DECARBOXYLASE.
GNC-25 OR Y37D8A.23.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditidae;
OC Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL.
RX MEDLINE: 99098940.
RA JIN Y., JORGENSEN E., HARTWIG E., HORVITZ H.R.:
RT "The Caenorhabditis elegans gene unc-25 encodes glutamic acid
RT decarboxylase and is required for synaptic transmission but not
RT synaptic development."
RT J. Neurosci. 19:539-548(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=C.elegans;
RX BAKLOW K.:
RX Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES=C.elegans;
RX MEDLINE: 94150718.
RA WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
RA BONFIELD J., BURTON J., CONNELL M., CORSEY T., COOPER J., COULSON A.,
RA CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
RA GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
RA JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LARRELLE P.,
RA LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
RA PARSONS J., PERCY C., RIFEEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
RA SMALLDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
RA THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
RA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.:
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans."
RT Nature 368:32-38(1994).
RL EMBL: AF109378; AAD19958.1; -.
DR EMBL: AL032626; CAA21537.1; -.
SQ SEQUENCE 508 AA; 57792 MW; 3A3E7F33 CRC32;

Query Match 65.3%; Score 96; DB 5; Length 508;
Best Local Similarity 57.9%; Pred. No. 4,48e-06;
Matches 11; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

Db 91 LRLGVTGHPREFNQISG 109
QY 2 LKVAIKTGHPRYFNQSTG 20

RESULT 12
ID 024062 PRELIMINARY; PRT; 575 AA.
AC 024062;
DT 01-NOV-1996 (TEMBLrel. 01, Created)
DT 01-NOV-1998 (TEMBLrel. 01, last sequence update)
DT 01-NOV-1998 (TEMBLrel. 08, last annotation update)
DE GLUTAMATE DECARBOXYLASE.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-OREGON-R; TISSUE-NEURAL;
RA PHILLIPS M., SAIKOFF L., KELLY L.:
RA J. Neurochem. 0:0-0(0);
DR EMBL: U01239; AAC4646.1; -.
DR FLYBASE: FBgn0005622; Gad2.
DR PFAM: PF00282; Pyridoxal dec. 1.
SQ SEQUENCE 575 AA; 64795 MW; 3CFA48E5 CRC32;

Query Match 59.2%; Score 87; DB 5; Length 575;
```

```
Best Local Similarity 50.0%; Pred. No. 6.52e-06;
Matches 10; Conservative 8; Mismatches 2; Indels 0; Gaps 0;

Db 156 TIRSVKTHPRFINDYSG 175
QY 1 LKVAIKTGHPRYFNQSTG 20

RESULT 13
ID 043308 PRELIMINARY; PRT; 1224 AA.
AC 043308;
DT 01-JUN-1998 (TEMBLrel. 06, Created)
DT 01-JUN-1998 (TEMBLrel. 06, last sequence update)
DT 01-AUG-1998 (TEMBLrel. 07, last annotation update)
DE KIAA0425.
GNC KIAA0425.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RA ISHIKAWA K., NAGASE T., NAKAJIMA D., SEKI N., OHIRA M., MIYAJIMA N.,
RA TANAKA A., KOTANI H., NOMURA N., OHARA O.:
RA Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB007885; BAA24855.1; -.
SQ SEQUENCE 1224 AA; 136329 MW; 8E27BD0D CRC32;

Query Match 46.3%; Score 68; DB 4; Length 1224;
Best Local Similarity 47.1%; Pred. No. 1.11e-01;
Matches 8; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

Db 1089 TLKSTKMTLRFPPPL 1105
QY 1 LKVAIKTGHPRYFNQ 17

RESULT 14
ID 09W668 PRELIMINARY; PRT; 77 AA.
AC 09W668;
DT 01-NOV-1999 (TEMBLrel. 12, Created)
DT 01-NOV-1999 (TEMBLrel. 12, last sequence update)
DT 01-NOV-1999 (TEMBLrel. 12, last annotation update)
DE MATRIX GLA PROTEIN (FRAGMENT).
GN MGP.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Amphibia;
OC Batrachia; Anura; Mesobatrachia; Pipidae; Pipodae; Xenopodinae;
OC Xenopus.
RN [1]
RP SEQUENCE FROM N.A.
RA CANCELA M.L.:
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF055586; AAD28354.1; -.
FT NON_TER
SQ SEQUENCE 77 AA; 9406 MW; 3DB2A863 CRC32;

Query Match 45.6%; Score 67; DB 13; Length 77;
Best Local Similarity 37.5%; Pred. No. 1.79e-01;
Matches 6; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

Db 56 ALRYGFTAAKRYFGQ 71
QY 1 LKVAIKTGHPRYFNQ 16

RESULT 15
ID 029449 PRELIMINARY; PRT; 1149 AA.
AC 029449;
DT 01-NOV-1996 (TEMBLrel. 01, Created)
DT 01-JAN-1999 (TEMBLrel. 09, last sequence update)
DT 01-MAY-1999 (TEMBLrel. 10, last annotation update)
DE CHROMAFIN GRANULE ATPase II.
```

```

OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;
OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae;
OC Bovinae; Bos.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 96234315.
RA TANG X., HALLECK M.S., SCHLEGEL R.A., WILLIAMSON P.;
RT "A subfamily of P-type ATPases with aminophospholipid transporting
RT activity."
RL Science 272:1495-1497(1996).
DR EMBL: U51100; AAD03352.1;
DR PFAM: PF00122; E1-E2_ATPase; 4.
KW Hydrolase; Transmembrane; Phosphorylation; ATP-binding.
FT MOD_RES 409 409 PHOSPHORYLATION (PROBABLE).
SQ SEQUENCE 1149 AA: 130025 MW: 73850931 CRC32;

Query Match 44.2% Score 65; DB 6; Length 1149;
Best Local Similarity 50.08; Pred. No. 4.60e-01;
Matches 9; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Db 733 TLKYALTFGVQYFLDIA 750
QY 1 TLKYAIKTGHPRYFNQLS 18

```

Search completed: Tue Mar 7 21:34:11 2000  
 Job time : 12 secs.

**THIS PAGE BLANK (USPTO)**



```

##residues 1-585 #label ERL
##cross-references GB:M72422; NID:g204225; PIDN:AAA63488.1; PID:g204226
##experimental_source brain
#note the authors translated the codon GAT for residue 86 as
His, TCA for residue 198 as Ala, and CAG for residue
428 as Trp

REFERENCE
#authors A60888
#journal J. Neurosci. (1988) 8:2123-2130
#title Characterization of the proteins purified with monoclonal
antibodies to glutamic acid decarboxylase.
#cross-references MUID:88258610
#accession A60888
#status preliminary
#molecule_type protein
#residues 'V',191-194,'X',196-203,'XX',206-219,'X',225-234,'X',
'X',236-247,'X',249-266,'X',524-537,539-543,'V',547-549,
'X',551-553,'X',555-558 #label CHA
COMMENT This enzyme (GAD) catalyzes the formation of an inhibitory
neurotransmitter, gamma-aminobutyric acid, from L-glutamic acid;
it has several isoforms, each encoded by a separate gene.
CLASSIFICATION #superfamily human glutamate decarboxylase
KEYWORDS carbon-carbon lyase; carboxy-lyase; phosphoprotein; pyridoxal
phosphate
FEATURE
396 #binding_site pyridoxal phosphate (lys) (covalent)
#status predicted
SUMMARY #length 585 #molecular_weight 65402 #checksum 7756

Query Match 100.0%; Score 155; DB 1; Length 585;
Best Local Similarity 100.0%; Pred. No. 3,18e-19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 176 PRYFMOLSTGLDMVGLADW 195
|||||
Oy 1 PRYFMOLSTGLDMVGLADW 20

RESULT 3
ENTRY A41292 #type complete
ENTRY glutamate decarboxylase (EC 4.1.1.15) 2 - human
TITLE glutamate decarboxylase GAD65; L-glutamate 1-carboxy-lyase
ALTERNATE_NAMES #formal_name Homo sapiens #common_name man
ORGANISM 13-May-1992 #sequence_revision 23-Mar-1995 #text_change
DATE 18-Jun-1999
ACCESSIONS A41935; A41292; S30058; B54778
REFERENCE A41935
#authors Bu, D.F.; Erlender, M.G.; Hiltz, B.C.; Tilkakaratne, N.J.K.;
Kaufman, D.L.; Wagner-McPherson, C.B.; Evans, G.A.; Tobin,
A.J.
#journal Proc. Natl. Acad. Sci. U.S.A. (1992) 89:2115-2119
#title Two human glutamate decarboxylases, 65-kDa GAD and 67-kDa
GAD, are each encoded by a single gene.
#cross-references MUID:92196068
#accession A41935
#molecule_type mRNA
#residues 1-585 #label BU1
#cross-references GB:M81882; NID:g182933; PIDN:AAA62367.1; PID:g182934
#experimental_source brain
#note #sequence extracted from NCHI backbone (NCBI:88007)
REFERENCE A41292
#authors Karlsson, A.E.; Hagopian, W.A.; Grubin, C.E.; Dube, S.;
Distcheche, C.M.; Adler, D.A.; Baermeier, H.; Mathewes, S.;
Grant, F.J.; Foster, D.; Lernermark, A.
#journal Proc. Natl. Acad. Sci. U.S.A. (1991) 88:8337-8341
#title Cloning and primary structure of a human islet isoform of
glutamic acid decarboxylase from chromosome 10.
#cross-references MUID:92020848
#accession A41292
#molecule_type mRNA
#residues 1-585 #label KAR
#cross-references GB:M74826; NID:g182931; PIDN:AAA58491.1; PID:g182932
#experimental_source pancreatic islet

```

```

REFERENCE
#authors S30058
#journal Mauch, L.; Abney, C.C.; Berg, H.; Scherbaum, W.A.; Liedvogel,
Eur. J. Biochem. (1993) 212:597-603
#title Characterization of a linear epitope within the human
pancreatic 64-kDa glutamic acid decarboxylase and its
autoimmune recognition by sera from insulin-dependent
diabetes mellitus patients.
#cross-references MUID:93185681
#accession S30058
#molecule_type mRNA
#residues 6-585 #label MAU
#cross-references EMBL:X69336
#experimental_source pancreatic islet
REFERENCE A54778
#authors Bu, D.F.; Tobin, A.J.
#journal Genomics (1994) 21:222-228
#title The exon-intron organization of the genes (GAD1 and GAD2)
encoding two human glutamate decarboxylases (GAD-67 and
GAD-65) suggests that they derive from a common ancestral
GAD.
#cross-references MUID:94375018
#contents annotation: intron-exon boundaries
COMMENT This enzyme (GAD) catalyzes the formation of an inhibitory
neurotransmitter, gamma-aminobutyric acid, from L-glutamic acid;
it has several isoforms, each encoded by a separate gene. GAD has
also been implicated as an autoantigen in autoimmune disease
stiff-man syndrome and insulin-dependent diabetes mellitus.
GENETICS
#gene GDB:GAD2
#cross-references GDB:128595; OMIM:138275
#map_position 10p11.23-10p11.23
CLASSIFICATION #superfamily human glutamate decarboxylase
KEYWORDS carbon-carbon lyase; carboxy-lyase; phosphoprotein; pyridoxal
phosphate
FEATURE
396 #binding_site pyridoxal phosphate (lys) (covalent)
#status predicted
SUMMARY #length 585 #molecular_weight 65411 #checksum 4799

Query Match 100.0%; Score 155; DB 1; Length 585;
Best Local Similarity 100.0%; Pred. No. 3,18e-19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 176 PRYFMOLSTGLDMVGLADW 195
|||||
Oy 1 PRYFMOLSTGLDMVGLADW 20

RESULT 4
ENTRY S38533 #type complete
ENTRY glutamate decarboxylase (EC 4.1.1.15) 2 - mouse
TITLE glutamate decarboxylase GAD65; L-glutamate 1-carboxy-lyase
ALTERNATE_NAMES #formal_name Mus musculus #common_name house mouse
ORGANISM 20-May-1994 #sequence_revision 23-Mar-1995 #text_change
DATE 18-Jun-1999
ACCESSIONS S38533
REFERENCE S38533
#authors Lee, D.S.; Tian, J.; Phan, T.; Kaufman, D.L.
#journal Biochim. Biophys. Acta (1993) 1216:157-160
#title Cloning and sequence analysis of a murine cDNA encoding
glutamate decarboxylase (GAD65).
#cross-references MUID:94032481
#accession S38533
#status preliminary
#molecule_type mRNA
#residues 1-585 #label IEE
#cross-references GB:U15980; NID:g413867; PIDN:AAA93049.1; PID:g413868
COMMENT This enzyme (GAD) catalyzes the formation of an inhibitory
neurotransmitter, gamma-aminobutyric acid, from L-glutamic acid;
it has several isoforms, each encoded by a separate gene.
CLASSIFICATION #superfamily human glutamate decarboxylase
KEYWORDS carbon-carbon lyase; carboxy-lyase; phosphoprotein; pyridoxal

```



FEATURE phosphate  
396 #binding\_site pyridoxal phosphate (Lys) (covalent)  
#status Predicted  
SUMMARY #length 585 #molecular-weight 65224 #checksum 7599

Query Match 100.0%; Score 155; DB 1; Length 585;  
Best Local Similarity 100.0%; Pred. No. 3.18e-19;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 176 PRFYNOLSTGLDMVGLADW 195  
1 PRFYNOLSTGLDMVGLADW 20

RESULT 5  
ENTRY JC4064 #type complete  
TITLE glutamate decarboxylase (EC 4.1.1.15) 65K chain - pig  
ORANISM #formal\_name Sus scrofa domestica #common\_name domestic pig  
DATE 30-Jun-1995 #sequence\_revision 14-Jul-1995 #text\_change 22-Jun-1999

ACCESSIONS JC4064  
REFERENCE JC4064  
#authors Suzuki, R.; Asami, N.; Amann, E.; Magatsuma, M.  
#journal Gene (1995) 152:257-260  
#title Sequences of two porcine glutamic acid decarboxylases (65-and 67-kDa GAD).

#cross-references MUID:95137399  
#accession JC4064  
#molecule\_type mRNA  
#residues 1-585 #label SUZ  
#cross-references DDBJ:D31848; NID:g790964; PIDN:BA06635.1;  
PID:d1007207; PID:g790965

COMMENT #experimental\_source brain  
This enzyme catalyzes the conversion of glutamic acid into gamma-amino butyric acid.

CLASSIFICATION #superfamily human glutamate decarboxylase  
KEYWORDS carbon-carbon lyase; carboxy-lyase  
FEATURE 393-396 #domain DOPA decarboxylase binding #status predicted  
#label BIN  
SUMMARY #length 585 #molecular-weight 65388 #checksum 5933

Query Match 100.0%; Score 155; DB 2; Length 585;  
Best Local Similarity 100.0%; Pred. No. 3.18e-19;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 176 PRFYNOLSTGLDMVGLADW 195  
1 PRFYNOLSTGLDMVGLADW 20

RESULT 6  
ENTRY I59173 #type complete  
TITLE glutamate decarboxylase - rat  
ORANISM #formal\_name Rattus norvegicus #common\_name Norway rat  
DATE 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 22-Jun-1999

ACCESSIONS I59173  
REFERENCE I59173  
#authors Bond, R.W.; Wyboriski, R.J.; Gottlieb, D.I.  
#journal Proc. Natl. Acad. Sci. U.S.A. (1990) 87:8771-8775  
#title Developmentally regulated expression of an exon containing a stop codon in the gene for glutamic acid decarboxylase.

#cross-references MUID:91062362  
#accession I59173  
#status preliminary; translated from GB/EMBL/DBJ  
#molecule\_type mRNA  
#residues 1-223 #label RES  
#cross-references GB:M38350; NID:g204231; PIDN:AAA41185.1; PID:g204232

CLASSIFICATION #superfamily human glutamate decarboxylase  
SUMMARY #length 223 #molecular-weight 25069 #checksum 1388

Query Match 87.1%; Score 135; DB 2; Length 223;  
Best Local Similarity 75.0%; Pred. No. 1.57e-14;  
Matches 15; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Db 184 PRFYNOLSTGLDMVGLADW 203  
1 PRFYNOLSTGLDMVGLADW 20

RESULT 7  
ENTRY S61534 #type complete  
TITLE glutamate decarboxylase (EC 4.1.1.15) 62K isoform - mouse  
ALTERNATE\_NAMES glutamic acid decarboxylase  
ORANISM #formal\_name Mus musculus #common\_name house mouse  
DATE 19-Mar-1997 #sequence\_revision 25-Apr-1997 #text\_change 22-Jun-1999

ACCESSIONS S61534  
REFERENCE S61534  
#authors Katarova, Z.; Szabo, G.; Mugnaini, E.; Greenspan, R.J.  
#journal Eur. J. Neurosci. (1990) 2:190-202  
#title Molecular identification of the 62 kd form of glutamic acid decarboxylase from the mouse.

#accession S61534  
#molecule\_type mRNA  
#residues 1-585 #label KAT  
#cross-references EMBL:Z49976  
#experimental\_source brain  
REFERENCE S61533  
#authors Szabo, G.  
#submission submitted to the EMBL Data Library, June 1995  
#accession S61533  
#molecule\_type mRNA  
#residues 1-554, 'YQPGDKANFRMYISNPASQSDIDFLTEIERLGDL' #label SZA

#cross-references EMBL:Z49976; NID:g886686; PIDN:CA90277.1;  
PID:g886687

COMMENT #experimental\_source brain  
#note the differences at the carboxyl end are due to a frameshift error

CLASSIFICATION #superfamily human glutamate decarboxylase  
KEYWORDS carbon-carbon lyase; carboxy-lyase  
SUMMARY #length 585 #molecular-weight 65381 #checksum 5716

Query Match 87.1%; Score 135; DB 2; Length 585;  
Best Local Similarity 75.0%; Pred. No. 1.57e-14;  
Matches 15; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Db 184 PRFYNOLSTGLDMVGLADW 203  
1 PRFYNOLSTGLDMVGLADW 20

RESULT 8  
ENTRY A41367 #type complete  
TITLE glutamate decarboxylase (EC 4.1.1.15) 1 - rat  
ALTERNATE\_NAMES glutamate decarboxylase GAD67; L-glutamate 1-carboxy-lyase  
ORANISM #formal\_name Rattus norvegicus #common\_name Norway rat  
DATE 12-Jun-1992 #sequence\_revision 23-Mar-1995 #text\_change 18-Jun-1999

ACCESSIONS A41367  
REFERENCE A41367  
#authors Michelsen, B.K.; Petersen, J.S.; Boel, E.; Moldrup, A.; Dyberberg, T.; Madsen, O.D.  
#journal Proc. Natl. Acad. Sci. U.S.A. (1991) 88:8754-8758  
#title Cloning, characterization, and autoimmune recognition of rat islet glutamic acid decarboxylase in insulin-dependent diabetes mellitus.

#cross-references MUID:92020930  
#accession A41367  
#status preliminary  
#molecule\_type mRNA  
#residues 1-593 #label MIC  
#cross-references GB:M76177; NID:g204227; PIDN:AAA41184.1; PID:g204228

REFERENCE A43756  
#authors Wyborski, R.J.; Bond, R.W.; Gottlieb, D.I.  
#journal Brain Res. Mol. Brain Res. (1990) 8:193-198  
#title Characterization of a cDNA coding for rat glutamic acid  
decarboxylase.  
#cross-references MUID:91014554  
#accession A43756  
#status Preliminary  
##molecule-type mRNA  
##residues 1-593 ##label WYB  
##cross-references GB:X57573; NID:956183; PIDN:CAA0801.1; PID:956184  
##note The authors translated the codon TGT for residue 412 as  
Ser and TCT for residue 413 as Cys

REFERENCE JH0195  
#authors Julien, J.F.; Samama, P.; Mallet, J.  
#journal J. Neurochem. (1990) 54:703-705  
#title Rat brain glutamic acid decarboxylase sequence deduced from a  
cloned cDNA.  
#cross-references MUID:90132703  
#accession JH0195  
##molecule-type mRNA  
##residues 1-102, 'V', '104-283', 'S', '285-286', 'AD', '289-343', 'EA', '346', 'I',  
348-351, 'LE', '354-379', 'R', '381-593' ##label JUL  
#cross-references GB:X57572; NID:956185; PIDN:CAA0800.1; PID:956186  
COMMENT This enzyme (GAD) catalyzes the formation of an inhibitory  
neurotransmitter, gamma-aminobutyric acid, from L-glutamic acid;  
it has several isoforms, each encoded by a separate gene.

CLASSIFICATION #superfamily human glutamate decarboxylase  
KEYWORDS carbon-carbon lyase; carboxy-lyase; phosphoprotein; pyridoxal  
phosphate

FEATURE 404  
#binding-site pyridoxal phosphate (Lys) (covalent)  
#status predicted

SUMMARY #length 593 #molecular-weight 66640 #checksum 3971  
#status predicted

Query Match 87.1%; Score 135; DB 1; Length 593;  
Best Local Similarity 75.0%; Pred. No. 1.57e-14;  
Matches 15; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Db 184 PRFNOLSTGLDVLGADW 203  
||:|||||||:||||:|

Qy 1 PRFNOLSTGLDVLGADW 20

RESULT 9  
ENTRY S48135 #type complete  
TITLE glutamate decarboxylase (EC 4.1.1.15) - human  
ORGANISM #formal\_name Homo sapiens #common\_name man  
DATE 14-Jul-1995 #sequence\_revision 10-Nov-1995 #text\_change  
07-May-1999

ACCESSIONS S48135  
REFERENCE S48135  
#authors Kelly, C.D.; Edwards, Y.; Johnstone, A.P.; Harfitt, E.;  
Nogradi, A.; Nussey, S.S.; Povey, S.; Carter, N.D.  
#journal Ann. Hum. Genet. (1992) 56:255-265  
#title Nucleotide sequence and chromosomal assignment of a cDNA  
encoding the large isoform of human glutamate  
decarboxylase.  
#cross-references MUID:93080286  
#accession S48135  
##molecule-type mRNA  
##residues 1-593 ##label KEL  
#cross-references EMBL:222750  
CLASSIFICATION #superfamily human glutamate decarboxylase  
KEYWORDS carbon-carbon lyase; carboxy-lyase  
SUMMARY #length 593 #molecular-weight 66952 #checksum 4836

Query Match 87.1%; Score 135; DB 2; Length 593;  
Best Local Similarity 75.0%; Pred. No. 1.57e-14;  
Matches 15; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Db 184 PRFNOLSTGLDVLGADW 203  
||:|||||||:||||:|

Qy 1 PRFNOLSTGLDVLGADW 20

RESULT 10  
ENTRY S51776 #type complete  
TITLE glutamate decarboxylase (EC 4.1.1.15) - human  
ORGANISM #formal\_name Homo sapiens #common\_name man  
DATE 15-Jul-1995 #sequence\_revision 21-Jul-1995 #text\_change  
16-Feb-1997

ACCESSIONS S51776  
REFERENCE S51775  
#authors Johnstone, A.  
#submission submitted to the EMBL Data Library, May 1993  
#accession S51776  
##status Preliminary  
##molecule-type mRNA  
##residues 1-593 ##label JOH  
##cross-references EMBL:222750  
##note this is an unpublished revision to the sequence from  
reference S48135

CLASSIFICATION #superfamily human glutamate decarboxylase  
KEYWORDS carbon-carbon lyase; carboxy-lyase  
SUMMARY #length 593 #molecular-weight 66946 #checksum 4842

Query Match 87.1%; Score 135; DB 2; Length 593;  
Best Local Similarity 75.0%; Pred. No. 1.57e-14;  
Matches 15; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Db 184 PRFNOLSTGLDVLGADW 203  
||:|||||||:||||:|

Qy 1 PRFNOLSTGLDVLGADW 20

RESULT 11  
ENTRY B41935 #type complete  
TITLE glutamate decarboxylase (EC 4.1.1.15) 1 - human  
ALTERNATE\_NAMES glutamate decarboxylase GAD67; L-glutamate 1-carboxy-lyase  
ORGANISM #formal\_name Homo sapiens #common\_name man  
DATE 31-Dec-1993 #sequence\_revision 23-Mar-1995 #text\_change  
18-Jun-1999

ACCESSIONS B41935; JH0805; A61406; PQ0157; PQ0158; B41367;  
B41935; JH0805; A54778  
REFERENCE A41935  
#authors Bu, D.F.; Erlander, M.G.; Hitz, B.C.; Tillakaratne, N.J.K.;  
Kaufman, D.L.; Wagner-McPherson, C.B.; Evans, G.A.; Tobin,  
A.J.  
Proc. Natl. Acad. Sci. U.S.A. (1992) 89:2115-2119  
#journal Two human glutamate decarboxylases, 65-kDa GAD and 67-kDa  
GAD, are each encoded by a single gene.  
#cross-references MUID:92196068  
#accession B41935  
##molecule-type mRNA  
##residues 1-594 ##label BUI  
#cross-references GB:M81883; NID:9182935; PIDN:AAA62368.1; PID:9182936  
##experimental\_source pancreatic islet  
##note sequence extracted from NCBI backbone (NCBIP:88006)

REFERENCE JH0805  
#authors Kawasaki, E.; Moriuchi, R.; Watanabe, M.; Saitoh, K.; Charles  
Brunicaudi, F.; Watt, P.C.; Yamaguchi, T.; Mullen, Y.;  
Akazawa, S.; Miyamoto, T.; Nagataki, S.  
#journal Biochem. Biophys. Res. Commun. (1993) 192:1353-1359  
#title Cloning and expression of large isoform of glutamic acid  
decarboxylase from human pancreatic islet.  
#cross-references MUID:93282845  
#accession JH0805  
##molecule-type mRNA  
##residues 1-17, 'N', '19-30', 'N', '32-67', 'K', '69-115', 'L', '117-154', 'T',  
156-301, 'C', '303-476', 'G', '478-491', 'G', '493-594' ##label  
KAW  
#cross-references GB:S61898; NID:9385310; PIDN:AA26938.1; PID:9385311  
#experimental\_source pancreatic islet  
REFERENCE JH0806  
#authors Yamashita, K.; Cram, D.S.; Harrison, L.C.

GENETICS

```
#journal      Biochem. Biophys. Res. Commun. (1993) 192:1347-1352
#title        Molecular cloning of full-length glutamic acid decarboxylase
              67 from human pancreas and islets.
#cross-references MUID:93282844
#accession    JH0806
##molecule_type mRNA
##residues    1-67, 'K', 69-435, 'L', 437-511, 'S', 513-594 ##label YKM
#cross-references GB:S61897; NID:q385450; PID:AA826937.1; PID:q385451
#experimental_source pancreatic islet
REFERENCE
#authors      Kelly, C.; Carter, N.D.; Johnstone, A.P.; Nussey, S.S.
#journal      Lancet (1991) 338:1468-1469
#title        Cloning of large isoform of human brain glutamic acid
              decarboxylase.
#cross-references MUID:92065769
#accession    A61406
##molecule_type mRNA
##residues    62-67, 'K', 69-205, 'N', 207-564, 'L', 566-594 ##label KEL
#experimental_source brain
REFERENCE
#authors      Gram, D.S.; Barnett, L.D.; Joseph, J.L.; Harrison, L.C.
#journal      Biochem. Biophys. Res. Commun. (1991) 176:1239-1244
#title        Cloning and partial nucleotide sequence of human glutamic
              acid decarboxylase cDNA from brain and pancreatic islets.
#cross-references MUID:91248209
#accession    P00157
##molecule_type mRNA
##residues    218-463 ##label CRL
#cross-references GB:M70434
#experimental_source brain
#accession    P00158
##molecule_type mRNA
#residues     218-234, 'K', 236-240, 'N', 242-288, 'H', 290-323, 'L', 325-329
              'D', 331-338, 'L', 340-390, 'S', 392-397 ##label CR2
#cross-references GB:M70435; NID:q182941; PID:AAA52513.1; PID:q182942
#experimental_source pancreatic islet
REFERENCE
#authors      Michelsen, B.K.; Petersen, J.S.; Boel, E.; Moldrup, A.;
              Dyrberg, T.; Madsen, O.D.
#journal      Proc. Natl. Acad. Sci. U.S.A. (1991) 88:8754-8758
#title        Cloning, characterization, and autoimmune recognition of rat
              islet glutamic acid decarboxylase in insulin-dependent
              diabetes mellitus.
#cross-references MUID:92020930
#accession    B41367
##molecule_type mRNA
#residues     317-482, 'R', 484-594 ##label MIC
REFERENCE
#authors      Persson, H.; Peltto-Huikko, M.; Metsis, M.; Soeder, O.; Brene
              S.; Skov, S.; Hoekfelt, T.; Ritzen, E.M.
#journal      Mol. Cell. Biol. (1990) 10:4701-4711
#title        Expression of the neurotransmitter-synthesizing enzyme
              glutamic acid decarboxylase in male germ cells.
#cross-references MUID:90355986
#accession    A36463
##molecule_type mRNA
##residues     527-594 ##label PBR
#cross-references GB:M55574; NID:q182929; PID:AAA72938.1; PID:q182930
REFERENCE
#authors      Bu, D.F.; Tobin, A.J.
#journal      Genomics (1994) 21:222-228
#title        The exon-intron organization of the genes (GAD1 and GAD2)
              encoding two human glutamate decarboxylases (GAD-67 and
              GAD-65) suggests that they derive from a common ancestral
              GAD.
#cross-references MUID:94375018
#contents     annotation: intron-exon organization
              This enzyme (GAD) catalyzes the formation of an inhibitory
              neurotransmitter, gamma-aminobutyric acid, from L-glutamic acid;
              it has several isoforms, each encoded by a separate gene. GAD has
              also been implicated as an autoantigen in autoimmune disease
              stiff-man syndrome and insulin-dependent diabetes mellitus.
```

```
#gene GDB:GAD1; GAD
#cross-references GDB:119244; OMIM:266100
#map_position 2q31-2q31
CLASSIFICATION #superfamily human glutamate decarboxylase
KEYWORDS alternative splicing; carbon-carbon lyase; carboxy-lyase;
phosphoprotein; pyridoxal phosphate
FEATURE
405 #binding-site pyridoxal phosphate (lys) (covalent)
SUMMARY #status predicted
#length 594 #molecular-weight 66924 #checksum 6189
Query Match 87.1%; Score 135; DB 1; Length 594;
Best Local Similarity 75.0%; Pred. No. 1,57e-14;
Matches 15; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Db 185 PRFNOLSTGLDMLAGLGEW 204
OY 1 PRFNOLSTGLDMLAGLGEW 20
RESULT 12
ENTRY #type complete
TITLE glutamate decarboxylase (EC 4.1.1.15) - human
ORGANISM Homo sapiens #common_name man
DATE 15-Jul-1995 #sequence_revision 21-Jul-1995 #text_change
22-Jun-1999
ACCESSIONS S51775
REFERENCE S51775
AUTHORS Johnstone, A.
SUBMISSION Submitted to the EMBL Data Library, May 1993
#accession S51775
STATUS Preliminary
#molecule_type mRNA
#residues 1-594 ##label JOH
#cross-references EMBL:Z22750; NID:g298098; PIDN:CAA80435.1;
PID:g298099
CLASSIFICATION #superfamily human glutamate decarboxylase
KEYWORDS carbon-carbon lyase; carboxy-lyase
SUMMARY #length 594 #molecular-weight 66973 #checksum 6437
Query Match 87.1%; Score 135; DB 2; Length 594;
Best Local Similarity 75.0%; Pred. No. 1,57e-14;
Matches 15; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Db 185 PRFNOLSTGLDITLAGLGEW 204
OY 1 PRFNOLSTGLDITLAGLGEW 20
ENTRY #type complete
TITLE glutamate decarboxylase (EC 4.1.1.15) 1 - cat
ALTERNATE_NAMES glutamate decarboxylase Gad67; L-glutamate 1-carboxy-lyase
ORIGIN #format_name Felis silvestris catus #common_name domestic cat
DATE 31-Dec-1993 #sequence_revision 23-Mar-1995 #text_change
18-Jun-1999
ACCESSIONS A46758; A45671#
REFERENCE A46758
AUTHORS Kobayashi, Y.; Kaufman, D.L.; Tobin, A.J.
SUBMISSION Submitted to GenBank, September 1989
#accession A46758
#molecule_type mRNA
##residues 1-594 ##label KOB
#cross-references GB:M18629; NID:g163858; PIDN:AAA51430.1; PID:g163859
REFERENCE A45671
AUTHORS Kobayashi, Y.; Kaufman, D.L.; Tobin, A.J.
J. Neurosci. (1987) 7:2768-2772
TITLE Glutamic acid decarboxylase cDNAs: nucleotide sequence
encoding an enzymatically active fusion protein.
#cross-references MJD:87310623
#accession A45671
#molecule_type mRNA
#residues 1-558; /RGTRPFGSGSSRPRIILHSPTTSSGRV; ##label KO2
```

#note this sequence has been revised in reference A46758  
COMMENT This enzyme (GAD) catalyzes the formation of an inhibitory neurotransmitter, gamma-aminobutyric acid, from L-glutamic acid; it has several isoforms, each encoded by a separate gene.

GENETICS  
#gene GAD1  
CLASSIFICATION #superfamily human glutamate decarboxylase  
KEYWORDS carbon-carbon lyase; carboxy-lyase; phosphoprotein; pyridoxal phosphate  
FEATURE 405 #binding-site pyridoxal phosphate (Lys) (covalent)  
#status predicted  
SUMMARY #length 594 #molecular-weight 66824 #checksum 5630

Query Match 87.1%; Score 135; DB 1; Length 594;  
Best Local Similarity 75.0%; Pred. No. 1.57e-14;  
Matches 15; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Db 185 PRFNOLSTGLDMVGLADW 204  
1 PRFNOLSTGLDMVGLADW 20

RESULT 14  
ENTRY JC4065 #type complete  
TITLE glutamate decarboxylase (EC 4.1.1.15) 67k chain - pig  
ORGANISM #formal\_name Sus scrofa domestica #common\_name domestic pig  
DATE 30-Jun-1995 #sequence\_revision 14-Jul-1995 #text\_change 22-Jun-1999

ACCESSIONS  
JC4065  
REFERENCE JC4064  
#authors Suzuki, R.; Asami, N.; Amann, E.; Wagatsuma, M.  
#journal Gene (1995) 152:257-260  
#title Sequences of two porcine glutamic acid decarboxylases (65- and 67-kDa GAD).  
#cross-references MUID:95137399  
#accession JC4065  
##molecule\_type mRNA  
##residues 1-594 #label SUZ  
##cross-references DDBJ:D31849; NID:g790966; PIDN:BAA06636.1; PID:d1007208; PID:g790967

COMMENT #experimental source brain  
This enzyme catalyzes the conversion of glutamic acid into gamma-amino butyric acid.  
CLASSIFICATION #superfamily human glutamate decarboxylase  
KEYWORDS carbon-carbon lyase; carboxy-lyase  
FEATURE 402-405 #domain DOPA decarboxylase binding #status predicted  
#label BIN  
SUMMARY #length 594 #molecular-weight 66894 #checksum 5491

Query Match 87.1%; Score 135; DB 2; Length 594;  
Best Local Similarity 75.0%; Pred. No. 1.57e-14;  
Matches 15; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Db 185 PRFNOLSTGLDMVGLADW 204  
1 PRFNOLSTGLDMVGLADW 20

RESULT 15  
ENTRY A30999 #type complete  
TITLE glutamate decarboxylase (EC 4.1.1.15) C1 - fruit fly  
(Drosophila melanogaster)  
ALTERNATE\_NAMES L-glutamate 1-carboxy-lyase  
ORGANISM #formal\_name Drosophila melanogaster  
DATE 26-Oct-1989 #sequence\_revision 23-Mar-1995 #text\_change 18-Jun-1999  
ACCESSIONS JH0192; PS0301; A30999  
REFERENCE JH0192  
#authors Jackson, F.R.; Newby, L.M.; Kulkarni, S.J.  
#journal J. Neurochem. (1990) 54:1068-1078  
#title Drosophila GABAergic systems; sequence and expression of

glutamic acid decarboxylase.  
#cross-references MUID:90155291  
#accession JH0192  
##molecule\_type mRNA  
##residues 1-510 #label JAC  
##cross-references GB:X76198; NID:q433082; PIDN:CA53791.1; PID:q433083  
#accession PS0301  
##molecule\_type mRNA  
##residues 156-200, 'F', 202-300, 'K', 302-384, 'L', 386-510 #label JAC  
COMMENT This enzyme (GAD) catalyzes the formation of an inhibitory neurotransmitter, gamma-aminobutyric acid, from L-glutamic acid; it has several isoforms, each encoded by a separate gene.

GENETICS  
#gene FlyBase:Gad1  
CLASSIFICATION #cross-references FlyBase:FBgn0004516  
KEYWORDS carbon-carbon lyase; carboxy-lyase; phosphoprotein; pyridoxal phosphate  
FEATURE 322 #binding-site pyridoxal phosphate (Lys) (covalent)  
#status predicted  
SUMMARY #length 510 #molecular-weight 57758 #checksum 3194

Query Match 74.2%; Score 115; DB 1; Length 510;  
Best Local Similarity 55.0%; Pred. No. 5.13e-10;  
Matches 11; Conservative 8; Mismatches 1; Indels 0; Gaps 0;

Db 102 PRFNOLSTGLDMVGLADW 121  
1 PRFNOLSTGLDMVGLADW 20

Search completed: Tue Mar 7 21:43:54 2000  
Job time : 8 secs.

\*\*\*\*\*  
[W][O][R][L][D]  
\*\*\*\*\*  
(TM)

Release 3.1a John F. Collins, Biocomputing Research Unit.  
Copyright (c) 1993-1998 University of Edinburgh, U.K.  
Distribution rights by Oxford Molecular Ltd

Merch\_pp protein - protein database search, using Smith-Waterman algorithm  
Run on: Tue Mar 7 21:41:36 2000; MasPar time 3.48 Seconds  
Tabular output not generated. 171.624 Million cell updates/sec

Title: >US-08-981-824-5  
Description: (1.20) From US08981824.pep  
Perfect Score: 155  
Sequence: 1 PRYFNUSTGLDMVGLADM 20

Scoring table: PAM 150  
Gap 15

Searched: 82229/seqs, 29864866 residues

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: swiss-prot38  
1:swissprot

Statistics: Mean 30.945; Variance 41.805; scale 0.740

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	155	100.0	585	1	DCE2_RAT GLUTAMATE DECARBOXYLASE	2.36e+21
2	155	100.0	585	1	DCE2_PIG GLUTAMATE DECARBOXYLASE	2.36e+21
3	155	100.0	585	1	DCE2_HUMAN GLUTAMATE DECARBOXYLASE	2.36e+21
4	155	100.0	585	1	DCE2_MOUSE GLUTAMATE DECARBOXYLASE	2.36e+21
5	135	87.1	593	1	DCE1_MOUSE GLUTAMATE DECARBOXYLASE	3.19e+16
6	135	87.1	593	1	DCE1_RAT GLUTAMATE DECARBOXYLASE	3.19e+16
7	135	87.1	594	1	DCE1_PIG GLUTAMATE DECARBOXYLASE	3.19e+16
8	135	87.1	594	1	DCE1_HUMAN GLUTAMATE DECARBOXYLASE	3.19e+16
9	135	87.1	594	1	DCE1_FELCA GLUTAMATE DECARBOXYLASE	3.19e+16
10	115	74.2	510	1	DCE_DROME GLUTAMATE DECARBOXYLASE	2.68e+11
11	65	41.9	325	1	MURE_PSEAE UDP-N-ACETYLMURAMOYLAL	1.58e+00
12	65	41.9	453	1	ASPARTATE AMINOTRANSFERASE	5.37e+00
13	62	40.0	344	1	MDH_METJA ASPARTATE AMINOTRANSFERASE	5.37e+00
14	62	40.0	405	1	ASPARTATE AMINOTRANSFERASE	5.37e+00
15	62	40.0	407	1	AATC_ORYSA ASPARTATE AMINOTRANSFERASE	5.37e+00
16	62	40.0	552	1	CHOD_BREST CHOLESTEROL OXIDASE PR	5.37e+00
17	61	39.4	360	1	HR38_BOMO PROBABLE NUCLEAR HOMO	7.98e+00
18	61	39.4	454	1	ALGC_PSEAE ASPARTATE AMINOTRANSFERASE	7.98e+00
19	61	39.4	462	1	ALGC_PSEAE PHOSPHOMANNOMUTASE (EC	7.98e+00
20	61	39.4	538	1	YABK_HAEN HYPOTHETICAL PROTEIN H	7.98e+00
21	60	38.7	221	1	YGIX_HAEN PROBABLE TRANSCRIPTION	1.18e+01
22	60	38.7	251	1	C561_HUMAN CYTOCHROME B561 (CYTOC	1.18e+01
23	60	38.7	384	1	VANS_ENTFC SENSOR PROTEIN VANS (E	1.18e+01

## ALIGNMENTS

RESULT	1	STANDARD	PRT	585 AA.
AC	005683:			
DT	01-FEB-1996 (Rel. 33, Created)			
DT	01-FEB-1996 (Rel. 33, Last sequence update)			
DI	01-FEB-1996 (Rel. 33, Last annotation update)			
DE	GLUTAMATE DECARBOXYLASE, 65 KD ISOFORM (EC 4.1.1.15) (GAD-65)			
GN	GAD5 OR GAD65			
OS	Rattus norvegicus (Rat).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;			
OC	Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			
RP	[1]			
RC	SEQUENCE FROM N.A.			
RC	TISSUE-HIPPOCAMPUS;			
RC	MEDLINE: 91299343.			
RA	ERLANDER M.G., TILAKARATNE N.J., FELDBLUM S., PATEL N.,			
RA	TOBIN A.J.;			
RT	"Two genes encode distinct glutamate decarboxylases.";			
RL	Neuron 7:91-100(1991).			
CC	-1- FUNCTION: CATALYZES THE PRODUCTION OF GABA.			
CC	-1- CATALYTIC ACTIVITY: L-GLUTAMATE = 4-AMINOBUTANOATE + CO(2).			
CC	-1- COFACTOR: PYRIDOXAL PHOSPHATE.			
CC	-1- SUBUNIT: HOMODIMER (BY SIMILARITY).			
CC	-1- SIMILARITY: LOCAL TO DOPA DECARBOXYLASE, AND TO PLP-TYPE HISTIDINE			
CC	DECARBOXYLASE.			
CC				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
CC	the European Bioinformatics Institute. There are no restrictions on its			
CC	use by non-profit institutions as long as its content is in no way			
CC	modified and this statement is not removed. Usage by and for commercial			
CC	entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a>			
CC	or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).			
DR	EMBL: M72422; AAA63488.1;			
DR	PROSITE: PS00392; DDC_GAD_HDC_YDC; 1.			
DR	PFAM: PF00282; pyridoxal_dec; 1.			
KW	Neurotransmitter biosynthesis; Lyase; Decarboxylase;			
KW	pyridoxal phosphate; Multiligene family.			
FT	BINDING 396 396 PYRIDOXAL PHOSPHATE (POTENTIAL).			
SQ	SEQUENCE 585 AA: 65402 MW: E35D601A CRC32;			

Query Match 100.0%; Score 155; DB 1; Length 585;  
Best Local Similarity 100.0%; Pred. No. 2.36e+21;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Db      176 PRYFNOLSTGLDMVGLADW 195
      |||||||
Oy      1 PRYFNOLSTGLDMVGLADW 20

RESULT  2
ID      DCE2_HUMAN      STANDARD:      PRT:      585 AA.
AC      P48321.
DT      01-FEB-1996 (Rel. 33, Created)
DT      01-FEB-1996 (Rel. 33, Last sequence update)
DT      01-FEB-1996 (Rel. 33, Last annotation update)
DE      GLUTAMATE DECARBOXYLASE, 65 KD ISOFORM (EC 4.1.1.15) (GAD-65)
DE      (65 KD GLUTAMIC ACID DECARBOXYLASE).
CN      GAD2 OR GAD65.
OS      Sus scrofa (Pig).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
      Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
RA      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE-BRAIN:
RX      MEDLINE: 95137399.
RA      SUZUKI R., ASAMI N., AMANN E., WAGATSUMA M.;
      "Sequences of two porcine glutamic acid decarboxylases (65- and
      67-kDa GAD).";
      Gene 152:257-260(1995).
RL      -1- FUNCTION: CATALYZES THE PRODUCTION OF GABA.
CC      -1- CATALYTIC ACTIVITY: L-GLUTAMATE = 4-AMINOBUTANOATE + CO(2).
CC      -1- COFACTOR: PYRIDOXAL PHOSPHATE.
CC      -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC      -1- SIMILARITY: BELONGS TO GROUP II DECARBOXYLASES (DDC, GAD, HDC AND
      TYRDC).
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
      between the Swiss Institute of Bioinformatics and the EMBL outstation -
      the European Bioinformatics Institute. There are no restrictions on its
      use by non-profit institutions as long as its content is in no way
      modified and this statement is not removed. Usage by and for commercial
      entities requires a license agreement (See http://www.isb-sib.ch/announce/
      or send an email to license@isb-sib.ch).
CC      -----
CC      EMBL: D31848; BAA06635.1; -.
DR      PROSITE: PS00392; DDC_GAD_HDC_YDC; 1.
DR      PIR: PF00282; pyridoxal dec; 1.
KW      Neurotransmitter biosynthesis; Lyase; Decarboxylase;
      KW      pyridoxal phosphate; Multigene family.
FT      BINDING 396 396 PYRIDOXAL PHOSPHATE (POTENTIAL).
SQ      SEQUENCE 585 AA: 65388 MW; F3E9BD88 CRC32;

Query Match      100.0%; Score 155; DB 1; Length 585;
Best Local Similarity 100.0%; Pred. No. 2,36e-21;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db      176 PRYFNOLSTGLDMVGLADW 195
      |||||||
Oy      1 PRYFNOLSTGLDMVGLADW 20

RESULT  3
ID      DCE2_HUMAN      STANDARD:      PRT:      585 AA.
AC      Q05329.
DT      01-FEB-1996 (Rel. 33, Created)
DT      01-FEB-1996 (Rel. 33, Last sequence update)
DT      01-FEB-1996 (Rel. 33, Last annotation update)
DE      GLUTAMATE DECARBOXYLASE, 65 KD ISOFORM (EC 4.1.1.15) (GAD-65)
DE      (65 KD GLUTAMIC ACID DECARBOXYLASE).
CN      GAD2 OR GAD65.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
      Eutheria; Primates; Catarrhini; Hominiidae; Homo.
RA      [1]
RP      SEQUENCE FROM N.A.
RC      MEDLINE: 92196068.
RX      BU D.-F., ERLANDER M.G., HITZ B.C., TILAKARATNE N.J., KAUFMAN D.L.,

```

```

RA      WAGNER-MCPHERSON C.B., EVANS G.A., TOBIN A.J.;
      "Two human glutamate decarboxylases, 65-kDa GAD and 67-kDa GAD, are
      each encoded by a single gene.";
      Proc. Natl. Acad. Sci. U.S.A. 89:2115-2119(1992).
RA      [2]
RP      SEQUENCE FROM N.A.
RC      MEDLINE: 94375018.
RX      BU D.-F., TOBIN A.J.;
      "The exon-intron organization of the genes (GAD1 and GAD2) encoding
      two human glutamate decarboxylases (GAD67 and GAD65) suggests that
      they derive from a common ancestral GAD.";
      Genomics 21:222-228(1994).
RA      [3]
RP      SEQUENCE FROM N.A.
RC      TISSUE-PANCREATIC ISLETS;
RX      MEDLINE: 92020848.
RA      KARLSEN A.E., HAGOPIAN W.A., GRUBIN C.E., DUBE S., DISTECHE C.M.,
      ADLER D.A., BARMEIER H., MATHIENES S., GRANT F.J., FOSTER D.,
      LERNMARK A.;
      "Cloning and primary structure of a human islet isoform of glutamic
      acid decarboxylase from chromosome 10.";
      Proc. Natl. Acad. Sci. U.S.A. 88:8337-8341(1991).
RA      [4]
RP      SEQUENCE OF 6-585 FROM N.A.
RC      TISSUE-PANCREAS;
RX      MEDLINE: 93185681.
RA      MAUCH L., ABNEY C.C., BERG H., SCHERBAUM W.A., LIEDVOGEL B.,
      NORTHEIMANN W.;
      "Characterization of a linear epitope within the human pancreatic
      64-kDa glutamic acid decarboxylase and its autoimmune recognition by
      sera from insulin-dependent diabetes mellitus patients.";
      Eur. J. Biochem. 212:597-603(1993).
CC      -1- FUNCTION: CATALYZES THE PRODUCTION OF GABA.
CC      -1- CATALYTIC ACTIVITY: L-GLUTAMATE = 4-AMINOBUTANOATE + CO(2).
CC      -1- COFACTOR: PYRIDOXAL PHOSPHATE.
CC      -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC      -1- SIMILARITY: LOCAL TO DOPA DECARBOXYLASE, AND TO PLP-TYPE HISTIDINE
      DECARBOXYLASE.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
      between the Swiss Institute of Bioinformatics and the EMBL outstation -
      the European Bioinformatics Institute. There are no restrictions on its
      use by non-profit institutions as long as its content is in no way
      modified and this statement is not removed. Usage by and for commercial
      entities requires a license agreement (See http://www.isb-sib.ch/announce/
      or send an email to license@isb-sib.ch).
CC      -----
CC      EMBL: M81882; AAA62367.1; -.
DR      EMBL: M74826; AAA58491.1; -.
DR      EMBL: X69936; CAA49554.1; ALT_INIT.
DR      EMBL: M70435; AAA52513.1; -.
DR      PIR: A41292; A41292.
DR      PIR: P00158; P00158.
DR      MIM: 138275; -.
DR      PROSITE: PS00392; DDC_GAD_HDC_YDC; 1.
DR      PIR: PF00282; pyridoxal dec; 1.
KW      Neurotransmitter biosynthesis; Lyase; Decarboxylase;
      KW      pyridoxal phosphate; Multigene family.
FT      BINDING 396 396 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
SQ      SEQUENCE 585 AA: 65411 MW; BAD62B62 CRC32;

Query Match      100.0%; Score 155; DB 1; Length 585;
Best Local Similarity 100.0%; Pred. No. 2,36e-21;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db      176 PRYFNOLSTGLDMVGLADW 195
      |||||||
Oy      1 PRYFNOLSTGLDMVGLADW 20

RESULT  4
ID      DCE2_MOUSE      STANDARD:      PRT:      585 AA.
AC      P48320; O35519;

```

DT 01-FEB-1996 (Rel. 33, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 15-JUL-1998 (Rel. 36, Last annotation update)  
 DE GLUTAMATE DECARBOXYLASE, 65 KD ISOFORM (EC 4.1.1.15) (GAD-65)  
 DE (65 KD GLUTAMIC ACID DECARBOXYLASE).  
 GN GAD2 OR GAD65.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 OC Eutheria; Rodentia; Sciurognathii; Muridae; Murinae; Mus.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-C57BL/6; TISSUE-BRAIN;  
 RX MEDLINE: 94032481.  
 RA LEE D.S., TIAN J., PHAN T., KAUFMAN D.L.;  
 RT "Cloning and sequence analysis of a murine cDNA encoding glutamate  
 decarboxylase (GAD65).";  
 RL Biochim. Biophys. Acta 1216:157-160(1993).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-C57BL/6; TISSUE-BRAIN;  
 RX MEDLINE: 97115675.  
 RA ASADA H., KAWAMURA Y., MARUYAMA K., KUME H., DING R.G., JI F.Y.,  
 RA KANBARA N., KUZUME H., SANBO M., YAGI T., OBARA K.;  
 RT "Mice lacking the 65 kDa isoform of glutamic acid decarboxylase  
 (GAD65) maintain normal levels of GAD67 and GABA in their brains but  
 are susceptible to seizures.";  
 RL Biochem. Biophys. Res. Commun. 229:891-895(1996).  
 RN [3]  
 RP SEQUENCE OF 175-379 FROM N.A.  
 RC TISSUE-BRAIN;  
 RX MEDLINE: 94062679.  
 RA FAULKNER-JONES B.E., GRAM D.S., KUN J., HARRISON L.C.;  
 RT "Localisation and quantitation of expression of two glutamate  
 decarboxylase genes in pancreatic beta-cells and other peripheral  
 tissues of mouse and rat.";  
 RL Endocrinology 133:2962-2972(1993).  
 CC - FUNCTION: CATALYZES THE PRODUCTION OF GABA.  
 CC - CATALYTIC ACTIVITY: L-GLUTAMATE = 4-AMINOBUTANOATE + CO(2).  
 CC - COFACTOR: PYRIDOXAL PHOSPHATE.  
 CC - SUBUNIT: HOMODIMER (BY SIMILARITY).  
 CC - SIMILARITY: LOCAL TO DOPA DECARBOXYLASE, AND TO PLP-TYPE HISTIDINE  
 DECARBOXYLASE.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL: L16980; AAA93049.1; -  
 CC EMBL: DA2051; BAA22893.1; -  
 CC EMBL: S67454; CAB32805.1; -  
 DR MGD: MGI:95634; GAD2.  
 DR PROSITE: PS00392; DDC\_GAD\_HDC\_YDC; 1.  
 DR PFAM: PF00282; Pyridoxal\_dec; 1.  
 KW Neurotransmitter biosynthesis; Lyase; Decarboxylase;  
 KM Pyridoxal phosphate; Multigene family;  
 -- BINDING 395  
 FT CONFLICT 259 395 PYRIDOXAL PHOSPHATE (POTENTIAL).  
 FT CONFLICT 319 319 I -> S (IN REF. 2).  
 FT CONFLICT 325 325 K -> E (IN REF. 2).  
 FT CONFLICT 499 499 P -> S (IN REF. 2).  
 SO SEQUENCE 585 AA; 65224 MW; 9B5C088 CRC32;

Query Match 100.0%; Score 155; DB 1; Length 585;  
 Best Local Similarity 100.0%; Pred. No. 2,36e-21;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 176 PRYFNOLSTGLDNGLAADW 195  
 |||  
 QY 1 PRYFNOLSTGLDNGLAADW 20

RESULT 5  
 ID DEEL\_MOUSE STANDARD; PRT; 593 AA.  
 AC P48318;  
 DT 01-FEB-1996 (Rel. 33, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DE GLUTAMATE DECARBOXYLASE, 67 KD ISOFORM (EC 4.1.1.15) (GAD-67)  
 DE (67 KD GLUTAMIC ACID DECARBOXYLASE).  
 GN GAD1 OR GAD67.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 OC Eutheria; Rodentia; Sciurognathii; Muridae; Murinae; Mus.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-BRAIN;  
 RA KATAROVA Z., SZABO G., MUGNANI E., GREENSPAN R.;  
 RT "Molecular identification of the 62 kd form of glutamic acid  
 decarboxylase from the mouse.";  
 RL Eur. J. Neurosci. 2:190-202(1990).  
 RN [2]  
 RP SEQUENCE OF 198-403 FROM N.A.  
 RC TISSUE-BRAIN;  
 RX MEDLINE: 94062679.  
 RA FAULKNER-JONES B.E., GRAM D.S., KUN J., HARRISON L.C.;  
 RT "Localisation and quantitation of expression of two glutamate  
 decarboxylase genes in pancreatic beta-cells and other peripheral  
 tissues of mouse and rat.";  
 RL Endocrinology 133:2962-2972(1993).  
 CC - FUNCTION: CATALYZES THE PRODUCTION OF GABA.  
 CC - CATALYTIC ACTIVITY: L-GLUTAMATE = 4-AMINOBUTANOATE + CO(2).  
 CC - COFACTOR: PYRIDOXAL PHOSPHATE.  
 CC - SUBUNIT: HOMODIMER (BY SIMILARITY).  
 CC - SIMILARITY: BELONGS TO GROUP II DECARBOXYLASES (DDC, GAD, HDC AND  
 TYRDC).  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL: Z49976; CAA90277.1; -  
 CC EMBL: S67453; CAB32805.1; -  
 DR MGD: MGI:95632; GAD1.  
 DR PROSITE: PS00392; DDC\_GAD\_HDC\_YDC; 1.  
 DR PFAM: PF00282; Pyridoxal\_dec; 1.  
 KW Neurotransmitter biosynthesis; Lyase; Decarboxylase;  
 KM Pyridoxal phosphate; Multigene family;  
 -- BINDING 404  
 FT CONFLICT 234 404 PYRIDOXAL PHOSPHATE (POTENTIAL).  
 FT CONFLICT 258 258 E -> K (IN REF. 2).  
 FT CONFLICT 360 360 S -> T (IN REF. 1).  
 FT CONFLICT 360 360 D -> S (IN REF. 1).  
 SO SEQUENCE 593 AA; 66584 MW; 63BC57AA CRC32;

Query Match 87.1%; Score 135; DB 1; Length 593;  
 Best Local Similarity 75.0%; Pred. No. 3,19e-16;  
 Matches 15; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Db 184 PRYFNOLSTGLDNGLAADW 203  
 |||  
 QY 1 PRYFNOLSTGLDNGLAADW 20

RESULT 6  
 ID DEEL\_RAT STANDARD; PRT; 593 AA.  
 AC P18088;  
 DT 01-NOV-1990 (Rel. 16, Created)  
 DT 01-NOV-1990 (Rel. 16, Last sequence update)  
 DT 01-FEB-1996 (Rel. 33, Last annotation update)

DT 01-FEB-1996 (Rel. 33, Last annotation update)

```

DE GLUTAMATE DECARBOXYLASE, 67 KD ISOFORM (EC 4.1.1.15) (GAD-67)
DE (67 KD GLUTAMIC ACID DECARBOXYLASE).
GN GAD1 OR GAD67.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 91014554.
RA WYBORSKI R.J., BOND R.W., GOTTLIEB D.I.;
RT "Characterization of a cDNA coding for rat glutamic acid
RT decarboxylase."
RL Brain Res. Mol. Brain Res. 8:193-198(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE: 90132703.
RA JULIEN J.F., SAMAMA P., MALLET J.;
RT "Rat brain glutamic acid decarboxylase sequence deduced from a cloned
RT cDNA."
RL J. Neurochem. 54:703-705(1990).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE: 92020930.
RA MICHELSEN B.K., PETERSEN J.S., BOEL E., MOLDROP A., DYRBERG T.,
RA MADSEN O.D.;
RT "Cloning, characterization, and autoimmune recognition of rat islet
RT glutamic acid decarboxylase in insulin-dependent diabetes mellitus."
RL Proc. Natl. Acad. Sci. U.S.A. 88:8754-8758(1991).
CC -1- FUNCTION: CATALYZES THE PRODUCTION OF GABA.
CC -1- CATALYTIC ACTIVITY: L-GLUTAMATE = 4-AMINOBUTANOATE + CO(2).
CC -1- COFACTOR: PYRIDOXAL PHOSPHATE.
CC -1- SUBUNIT: HOMODIMER.
CC -1- SIMILARITY: BELONGS TO GROUP II DECARBOXYLASES (DDC, GAD, HDC AND
CC TYRDC).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL: M34445; AAC42037.1; -
DR EMBL: X57572; CAA40800.1; -
DR EMBL: X57573; CAA40801.1; -
DR EMBL: M76177; AAA41184.1; -
DR PIR: A41367; A41367.
DR PIR: A43756; A43756.
DR PROSITE: PS00392; DDC_GAD_HDC_YDC; 1.
DR PFAM: PF00282; pyridoxal_dec; 1.
KW Neurotransmitter biosynthesis; Lyase; Decarboxylase;
KW pyridoxal phosphate; Multigene family.
FT BINDING 404 404 PYRIDOXAL PHOSPHATE (POTENTIAL).
FT CONFLICT 103 103 L -> V (IN REF. 2).
FT CONFLICT 284 284 F -> S (IN REF. 2).
FT CONFLICT 287 288 EH -> AD (IN REF. 2).
FT CONFLICT 344 345 AG -> EA (IN REF. 2).
FT CONFLICT 347 347 T -> I (IN REF. 2).
FT CONFLICT 352 353 FD -> LE (IN REF. 2).
FT CONFLICT 380 380 L -> R (IN REF. 2).
SQ SEQUENCE 593 AA: 66640 MW: 5A0B67C0 CRC32;

```

Query Match 87.1%; Score 135; DB 1; Length 593;

Best Local Similarity 75.0%; Pred. No. 3.19e-16;

Matches 15; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

```

Db 184 PRFNLSTGLDILIGAGEM 203
Oy 1 PRFNLSTGLDMVGLADW 20
RESULT 7

```

```

ID DCEL_PIG STANDARD; PRT: 594 AA.
AC P48319.
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE GLUTAMATE DECARBOXYLASE, 67 KD ISOFORM (EC 4.1.1.15) (GAD-67)
DE (67 KD GLUTAMIC ACID DECARBOXYLASE).
GN GAD1 OR GAD67.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE-BRAIN:
RX MEDLINE: 95137399.
RA SUZUKI R., ASAMI N., AMANN E., WAGATSUNA M.;
RT "Sequences of two porcine glutamic acid decarboxylases (65- and
RT 67-kDa GAD)."
RL Gene 152:257-260(1995).
CC -1- FUNCTION: CATALYZES THE PRODUCTION OF GABA.
CC -1- CATALYTIC ACTIVITY: L-GLUTAMATE = 4-AMINOBUTANOATE + CO(2).
CC -1- COFACTOR: PYRIDOXAL PHOSPHATE.
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO GROUP II DECARBOXYLASES (DDC, GAD, HDC AND
CC TYRDC).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL: D31849; BAA06636.1; -
DR PROSITE: PS00392; DDC_GAD_HDC_YDC; 1.
DR PFAM: PF00282; pyridoxal_dec; 1.
KW Neurotransmitter biosynthesis; Lyase; Decarboxylase;
KW pyridoxal phosphate; Multigene family.
FT BINDING 405 405 PYRIDOXAL PHOSPHATE (POTENTIAL).
FT PIR: A405 405 PYRIDOXAL PHOSPHATE (POTENTIAL).
SQ SEQUENCE 594 AA: 66894 MW: 69D6C79C CRC32;

```

Query Match 87.1%; Score 135; DB 1; Length 594;

Best Local Similarity 75.0%; Pred. No. 3.19e-16;

Matches 15; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

```

Db 185 PRFNLSTGLDILIGAGEM 204
Oy 1 PRFNLSTGLDMVGLADW 20
RESULT 8
ID DCEL_HUMAN STANDARD; PRT: 594 AA.
AC O99259.
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE GLUTAMATE DECARBOXYLASE, 67 KD ISOFORM (EC 4.1.1.15) (GAD-67)
DE (67 KD GLUTAMIC ACID DECARBOXYLASE).
GN GAD1 OR GAD.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominiidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE-BRAIN:
RX MEDLINE: 92196068.
RA BU D.-F., ERLANDER M.G., HITZ B.C., TILIAKARATNE N.J., KAUFMAN D.L.,
RA WAGNER-MCPHERSON C.B., EVANS G.A., TOBIN A.J.;
RT "Two human glutamate decarboxylases, 65-kDa GAD and 67-kDa GAD, are
RT each encoded by a single gene."
RL Proc. Natl. Acad. Sci. U.S.A. 89:2115-2119(1992).
RN [2]

```



RP SEQUENCE FROM N.A.  
 RX MEDLINE: 94375018.  
 RA BU D.-F., TOBIN A.J.;  
 RT "The exon-intron organization of the genes (GAD1 and GAD2) encoding  
 RT two human glutamate decarboxylases (GAD67 and GAD65) suggests that  
 RT they derive from a common ancestral GAD.";  
 RL Genomics 21:222-228(1994).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-BRAIN;  
 RX MEDLINE: 93080286.  
 RA KELLY C.D., EDWARDS Y., JOHNSTONE A.P., HARFEST E., NOGRADI A.,  
 RA NUSSEY S.S., POVEY S., CARTER N.D.;  
 RT "Nucleotide sequence and chromosomal assignment of a cDNA encoding  
 RT the large isoform of human glutamate decarboxylase.";  
 RL Ann. Hum. Genet. 56:255-265(1992).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE: 93282844.  
 RA YAMASHITA K., CRAW D.S., HARRISON L.C.;  
 RT "Molecular cloning of full-length glutamic acid decarboxylase 67 from  
 RT human pancreas and islets.";  
 RL Biochem. Biophys. Res. Commun. 192:1347-1352(1993).  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-PANCREATIC ISLETS;  
 RX MEDLINE: 93282845.  
 RA KAMASAKI E., MORIUCHI R., WATANABE M., SATOH K., BRUNICARDI F.C.,  
 RA KAITI P.C., YAMAGUCHI T., MULLEN Y., AKAZAWA S., MIYAMOTO T.;  
 RT "Cloning and expression of large isoform of glutamic acid  
 RT decarboxylase from human pancreatic islet.";  
 RL Biochem. Biophys. Res. Commun. 192:1353-1359(1993).  
 RN [6]  
 RP SEQUENCE FROM N.A.  
 RA GIORDA R., PEAKMAN M., VERGANI D., TRUCCO M.;  
 RT Submitted (MAR-1992) to the EMBL/GenBank/DBJ databases.  
 RL [7]  
 RP SEQUENCE OF 218-397 FROM N.A.  
 RC TISSUE-BRAIN;  
 RX MEDLINE: 91248209.  
 RA CRAW D.S., BARRETT L.D., JOSEPH J.L., HARRISON L.C.;  
 RT "Cloning and partial nucleotide sequence of human glutamic acid  
 RT decarboxylase cDNA from brain and pancreatic islets.";  
 RL Biochem. Biophys. Res. Commun. 176:1239-1244(1991).  
 RN [8]  
 RP SEQUENCE OF 527-594 FROM N.A.  
 RC TISSUE-TESTIS;  
 RX MEDLINE: 90355986.  
 RA PERSSON H., PELTO-HUINKO M., METSIS M., SOEDER O., BRENE S.,  
 RA SKOG S., HOEKFELT T., RITZEN E.M.;  
 RT "Expression of the neurotransmitter-synthesizing enzyme glutamic acid  
 RT decarboxylase in male germ cells.";  
 RL Mol. Cell. Biol. 10:4701-4711(1990).  
 CC -1- FUNCTION: CATALYZES THE PRODUCTION OF GABA.  
 CC -1- CATALYTIC ACTIVITY: L-GLUTAMATE + CO(2).  
 CC -1- COFACTOR: PYRIDOXAL PHOSPHATE.  
 CC -1- SUBUNIT: HOMODIMER.  
 CC -1- SIMILARITY: BELONGS TO GROUP II DECARBOXYLASES (DDC, GAD, HDC AND  
 CC TYRDC).  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL: M81883: AAA62368.1: -  
 CC EMBL: L16888: AAB59427.1: -  
 CC EMBL: 222750: CAAB0435.1: -  
 CC EMBL: S61897: AAB26937.1: -  
 CC EMBL: S61898: AAB26938.1: -

DR EMBL: M86522: AAA35900.1: -  
 DR EMBL: M70434: AAA52512.1: -  
 DR EMBL: M55574: AAA72938.1: -  
 DR EMBL: A28074: CAAB0435.1: -  
 DR PIR: P00157: P00157.  
 DR MIM: 266100: -  
 DR PROSITE: PS00392; DDC\_GAD\_HDC\_YDC: 1.  
 DR PFAM: PF00282; pyridoxal\_dec: 1.  
 KW Neurotransmitter biosynthesis; Lyase; Decarboxylase;  
 KW Pyridoxal phosphate; Multigene family.  
 FT BINDING 405  
 FT CONFLICT 9  
 FT CONFLICT 16  
 FT CONFLICT 17  
 FT CONFLICT 17  
 FT CONFLICT 18  
 FT CONFLICT 31  
 FT CONFLICT 31  
 FT CONFLICT 68  
 FT CONFLICT 116  
 FT CONFLICT 136  
 FT CONFLICT 140  
 FT CONFLICT 142  
 FT CONFLICT 142  
 FT CONFLICT 155  
 FT CONFLICT 206  
 FT CONFLICT 302  
 FT CONFLICT 436  
 FT CONFLICT 512  
 FT CONFLICT 477  
 FT CONFLICT 492  
 FT CONFLICT 565  
 FT CONFLICT 565  
 SQ SEQUENCE 594 AA: 66896 MW: 94733552 CRC32:  
 Query Match 87.1%; Score 135; DB 1; Length 594;  
 Best Local Similarity 75.0%; Pred. No. 3.19e-16;  
 Matches 15; Conservative 5; Mismatches 0; Indels 0; Gaps 0;  
 Db 185 PRFNOLSTGLDIITAGLGEW 204  
 QY 1 PRYFNOLSTGLDMVGLAADW 20  
 RESULT 9  
 ID DCE1\_FELCA STANDARD; PRT: 594 AA.  
 AC P14748;  
 DT 01-APR-1990 (Rel. 14, Created)  
 DT 01-OCT-1993 (Rel. 27, Last sequence update)  
 DT 01-FEB-1996 (Rel. 33, Last annotation update)  
 DE GLUTAMATE DECARBOXYLASE, 67 KD ISOFORM (EC 4.1.1.15) (GAD-67)  
 DE (67 KD GLUTAMIC ACID DECARBOXYLASE).  
 GN GAD1 OR GAD67.  
 OS Felis silvestris catus (Cat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 OC Eutheria; Carnivora; Fissipedia; Felidae; Felis.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-OCIPITAL CORTEX;  
 RX MEDLINE: 87310623.  
 RA KOBAYASHI Y., KAUFMAN D.L., TOBIN A.J.;  
 RT "Glutamic acid decarboxylase cDNA: nucleotide sequence encoding an  
 RT enzymatically active fusion protein.";  
 RL J. Neurosci. 7:2768-2772(1987).  
 CC -1- FUNCTION: CATALYZES THE PRODUCTION OF GABA.  
 CC -1- CATALYTIC ACTIVITY: L-GLUTAMATE + CO(2).  
 CC -1- COFACTOR: PYRIDOXAL PHOSPHATE.  
 CC -1- SUBUNIT: HOMODIMER.  
 CC -1- SIMILARITY: BELONGS TO GROUP II DECARBOXYLASES (DDC, GAD, HDC AND  
 CC TYRDC).  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>

```

CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: M18629; AAS1430.1; -
DR PIR: A45671; A45671.
DR PIR: A46758; A46758.
DR PROSITE: PS00392; DDC_GAD_HDC_YDC; 1.
DR PFAM: PF00282; pyridoxal_dec; 1.
DR Neurotransmitter biosynthesis; Lyase; Decarboxylase;
KW Pyridoxal phosphate; Multigene family.
FT BINDING 405 405 PYRIDOXAL PHOSPHATE (POTENTIAL).
SQ SEQUENCE 594 AA; 66824 MW; 3EC20778 CRC32;

Query Match 87.1%; Score 135; DB 1; Length 594;
Best Local Similarity 75.0%; Pred. No. 3.19e-16;
Matches 15; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Db 185 PRFNOLSTGLDMVGLADM 204
1 PRFNOLSTGLDMVGLADM 20

RESULT 10
ID DCE_DROME STANDARD: PRT; 510 AA.
AC P20228;
DT 01-FEB-1991 (Rel. 17, Created)
NM 01-FEB-1991 (Rel. 17, Last sequence update)
NT 01-NOV-1995 (Rel. 32, Last annotation update)
DE GLUTAMATE DECARBOXYLASE (EC 4.1.1.15) (GAD).
GN GAD OR GLB.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Ephydrota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
CC [1]
RN SEQUENCE FROM N.A.
RP MEDLINE: 90155291.
RX JACKSON F.R., NEMBY L.M., KULKARNI S.J.;
RT "Drosophila GABAergic systems: sequence and expression of glutamic
acid decarboxylase".
RL J. Neurochem. 54:1068-1078(1990).
CC -1- FUNCTION: CATALYZES THE PRODUCTION OF GABA.
CC -1- CATALYTIC ACTIVITY: L-GLUTAMATE -> 4-AMINOBUTANOATE + CO(2).
CC -1- COFACTOR: PYRIDOXAL PHOSPHATE.
CC -1- SUBUNIT: HOMODIMER.
CC -1- SIMILARITY: BELONGS TO GROUP II DECARBOXYLASES (DDC, GAD, HDC AND
TYRDC).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (see http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
CC -----
CC EMBL: X76198; CAAS3791.1; -
DR PIR: A30999; A30999.
DR PIR: JH0192; JH0192.
DR FLYBASE: FBgn0004516; Gad1.
DR PROSITE: PS00392; DDC_GAD_HDC_YDC; 1.
DR PFAM: PF00282; pyridoxal_dec; 1.
DR Neurotransmitter biosynthesis; Lyase; Decarboxylase;
KW Pyridoxal phosphate.
FT BINDING 322 322 PYRIDOXAL PHOSPHATE (POTENTIAL).
SQ SEQUENCE 510 AA; 57758 MW; 97C7A8F1 CRC32;

Query Match 74.2%; Score 115; DB 1; Length 510;
Best Local Similarity 55.0%; Pred. No. 2.68e-11;
Matches 11; Conservative 8; Mismatches 1; Indels 0; Gaps 0;

Db 102 PRFNOLSTGLDMVGLADM 121
1 PRFNOLSTGLDMVGLADM 20

```

```

RESULT 11
ID MURE_PSEAE STANDARD: PRT; 325 AA.
AC O59650;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE UDP-N-ACETYLURAMIDYL-L-D-GLUTAMATE--2,6-DIAMINOPIMELATE LIGASE
DE (EC 6.3.2.13) (UDP-N-ACETYLURAMYL-TRIPETIDE SYNTHETASE) (MESO-
DE DIMINOPIMELATE-ADDING ENZYME) (FRAGMENT).
GN MURE.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonas group;
OC Pseudomonas.
CC [1]
RN SEQUENCE FROM N.A.
RP STRAIN=ATCC 15692 / PAOI;
RX MEDLINE: 96100768.
RA LIAO X., HANCOCK R.E.W.;
RT "Cloning and characterization of the Pseudomonas aeruginosa pbpb gene
encoding penicillin-binding protein 3.".
RL Antimicrob. Agents Chemother. 39:1871-1874(1995).
CC -1- FUNCTION: CELL WALL FORMATION. DIAMINOPIMELIC ACID ADDING ENZYME.
CC -1- CATALYTIC ACTIVITY: ATP + UDP-N-ACETYLURAMOTL-L-ALANYL-D-
CC GLUTAMATE + MESO-2,6-DIAMINOHEPTANEDIOATE -> ADP + ORTHOPHOSPHATE
CC + UDP-N-ACETYLURAMOTYL-L-ALANYL-D-GLUTAMYL-MESO-2,6-
CC DIAMINOHEPTANEDIOATE.
CC -1- PATHWAY: PEPTIDOGLYCAN BIOSYNTHESIS.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (PROBABLE).
CC -1- SIMILARITY: BELONGS TO THE MURCEP FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (see http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X84053; CAAS8873.1; -
DR PFAM: PF01225; Mur_Ligase; 1.
KW Peptidoglycan synthesis; Cell wall; Cell division; Ligase;
KW ATP-binding.
FT NP_BIND 108 114 ATP (POTENTIAL).
FT NON_TER 325 325
SQ SEQUENCE 325 AA; 34215 MW; 442CD550 CRC32;

Query Match 41.9%; Score 65; DB 1; Length 325;
Best Local Similarity 35.3%; Pred. No. 1.58e+00;
Matches 6; Conservative 8; Mismatches 3; Indels 0; Gaps 0;

Db 92 RYFGEPSRGLDVGTVG 108
2 RYFNLSTGLDMVGLAA 18

RESULT 12
ID AATM_ARATH STANDARD: PRT; 453 AA.
AC P46248;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE ASPARTATE AMINOTRANSFERASE, MITOCHONDRIAL PRECURSOR (EC 2.6.1.1)
DE (TRANSMINASE A).
GN AAT1 OR ASP5.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Eukaryotes; Spermatophyta; Magnoliophyta; eudicotyledons;
OC core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
OC Arabidopsis.
RN [1]
RP SEQUENCE FROM N.A.

```

```

RC TISSUE-LEAF:
RA MILKIE S.E., ROBER J., SMITH A., WARREN M.J.;
RL Submitted (AUG-1994) to the EMBL/Genbank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-CV, LANDSBERG ERRECTA; TISSUE=LEAF;
RA MILKIE S.E., LAMBERT R., WARREN M.J.;
RL Submitted (SEP-1995) to the EMBL/Genbank/DBJ databases.
CC -1- FUNCTION: IMPORTANT FOR THE METABOLISM OF AMINO ACIDS AND KREBS-
CC CYCLE RELATED ORGANIC ACIDS. IN PLANTS, IT IS INVOLVED IN NITROGEN
CC METABOLISM AND IN ASPECTS OF CARBON AND ENERGY METABOLISM.
CC -1- CATALYTIC ACTIVITY: L-ASPARTATE + 2-OXOGLUTARATE = OXALOACETATE +
CC L-GLUTAMATE.
CC -1- COPACTOR: PYRIDOXAL PHOSPHATE.
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: MITOCHONDRIAL MATRIX (POTENTIAL).
CC -1- SIMILARITY: BELONGS TO CLASS-I OF PYRIDOXAL-PHOSPHATE-DEPENDENT
CC AMINOTRANSFERASES.
-----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
-----
DR EMBL; X81026; CAAG56932.1; -.
DR EMBL; X91865; CAA62972.1; -.
DR HSSP; P00508; ITAT.
DR PROSITE; PS00105; AA_TRANSFER.CLASS_1; 1.
DR PFAM; PF00155; aminotran_1; 1.
KW transferase; Aminotransferase; Pyridoxal phosphate; Mitochondrion;
KM transit peptide; Multigene family.
FT TRANSIT 1 52 MITOCHONDRION (POTENTIAL).
FT CHAIN 53 453 ASPARTATE AMINOTRANSFERASE.
FT BINDING 298 298 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
SQ SEQUENCE 453 AA: 49603 MW: 080381EA CRC32:

Query Match 41.9%; Score 65; DB 1; Length 453;
Best Local Similarity 44.4%; Pred. No. 1.58e+00;
Matches 8; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Db 199 RYDPKPTIGLDFEGMIAD 216
   ||| : ||| 1: 11
QY 2 RYFNQLSTGLDMVGSLAD 19

RESULT 13
ID MDH_MENJA STANDARD; PRT. 344 AA.
AC Q58820;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE MALATE DEHYDROGENASE (EC 1.1.1.37) (EC 1.1.1.82).
GN MDH OR MJ1425.
OS Methanococcus jannaschii.
OC Archaea; Euryarchaeota; Methanococcales; Methanococcaceae;
CC Methanococcus.
[1]
RP SEQUENCE FROM N.A.
RX STRAIN-JAL-1 / DSM 2661 / ATCC 43067;
RX MEDLINE; 96337999.
RA BULT C.J., WHITE O., OLSEN G.J., ZHOU L., FLEISCHMANN R.D.,
RA SUTTON G.G., BLAKE J.A., FITZGERALD L.M., CLAYTON R.A., GOCAINE J.D.,
RA KERDLAVAGE A.R., DOUGHERTY B.A., TOMB J.-F., ADAMS M.D., REICH C.I.,
RA OVERBEER K., KIRKNES E.F., WEINSTOCK K.G., MERRICK J.M., GLUCKER A.,
RA SCOTT J.L., GEOGAGNAN N.S.M., WEIDMAN J.F., FUHRMANN J.L., NGUYEN D.,
RA UTERBACK T.R., KELLEY J.M., PETERSON J.D., SAOW P.W., HANNA M.C.,
RA COTTON M.D., ROBERTS K.M., HURST M.A., KAINE B.P., BOBODOVSKY M.,
RA KLENK H.-P., FRASER C.M., SMITH H.O., WOESE C.R., VENTER J.C.;
RI "Complete genome sequence of the methanogenic archaeon, Methanococcus
jannaschii."

```

```

RL Science273:1058-1073(1996).
CC -1- CATALYTIC ACTIVITY: L-MALATE + NAD(+) = OXALOACETATE + NADH.
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE "ARCHAEBACTERIAL" MALATE DEHYDROGENASE
CC FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC DR EMBL: U67583; AAB99436.1; -.
CC KW Oxidoreductase; Tricarboxylic acid cycle; NAD.
CC FT ACT_SITE 186 186 PROTON-RELAY (POTENTIAL).
CC FT BINDING 189 189 SUBSTRATE CARBOXYL GROUP (POTENTIAL).
CC FT SEQUENCE 344 AA; 37358 MW; 457C3727 CRC32;
CC -----
Cc Db 122 YSELANMODMIGT 136
Cc Qy 3 YFNOLSTGLDMVGIA 17
Cc -----
Cc RESULT 14
Cc ID AAT2_ARATH STANDARD: PRI: 405 AA.
Cc AC P46645;
Cc DT 01-NOV-1995 (Rel. 32, Created)
Cc DT 01-NOV-1995 (Rel. 32, Last sequence update)
Cc DT 15-DEC-1998 (Rel. 37, Last annotation update)
Cc DE ASPARTATE AMINOTRANSFERASE, CYTOSOLIC ISOZYME 1 (EC 2.6.1.1)
Cc GN (TRANSMINASE A).
Cc GN Asp2.
Cc OS Arabidopsis thaliana (Mouse-ear cress).
Cc OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Cc OC euphylliphytes; Spermatophyta; Magnoliophyta; eudicotyledons;
Cc OC core eudicots; Rosidae; eustosids II; Brassicales; Brassicaceae;
Cc OC Arabidopsids.
Cc RN (1)
Cc RP SEQUENCE FROM N.A.
Cc RC STRAIN=CV, COLUMBIA; TISSUE=LEAF;
Cc RX MEDLINE: 95201829.
Cc RA SCHULTZ C.J., CORUZZI G.M.;
Cc RT "The aspartate aminotransferase gene family of Arabidopsis encodes
Cc RT isoenzymes localized to three distinct subcellular compartments.";
Cc RL Plant J. 7:61-75(1995).
Cc RN [2]
Cc RP SEQUENCE OF 327-405 FROM N.A.
Cc RC STRAIN=CV, COLUMBIA; TISSUE=LEAF;
Cc RA PARENTIER Y., CRIQUI M.C., DURR A., FLECK J.;
Cc RT Submitted (OCT-1993) to the EMBL/Genbank/DBJ databases.
Cc RL -1- FUNCTION: IMPORTANT FOR THE METABOLISM OF AMINO ACIDS AND KREBS-
Cc CC CYCLE RELATED ORGANIC ACIDS. IN PLANTS, IT IS INVOLVED IN NITROGEN
Cc CC METABOLISM AND IN ASPECTS OF CARBON AND ENERGY METABOLISM.
Cc CC -1- CATALYTIC ACTIVITY: L-ASPARTATE + 2-OXOGLOUTARATE = OXALOACETATE +
Cc CC L-GLUTAMATE.
Cc CC -1- COFACTOR: PYRIDOXAL PHOSPHATE.
Cc CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
Cc CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (POTENTIAL)..
Cc CC -1- SIMILARITY: BELONGS TO CLASS-I OF PYRIDOXAL-PHOSPHATE-DEPENDENT
Cc CC AMINOTRANSFERASES.
Cc -----
Cc This SWISS-PROT entry is copyright. It is produced through a collaboration
Cc between the Swiss Institute of Bioinformatics and the EMBL outstation -
Cc the European Bioinformatics Institute. There are no restrictions on its
Cc use by non-profit institutions as long as its content is in no way
Cc modified and this statement is not removed. Usage by and for commercial

```

CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

CC -----  
 DR EMBL: U15033; AAA79370.1; -  
 DR EMBL: Z26740; CAA8141.1; -  
 DR HSSP: P00508; ITAT.  
 DR PROSITE: PS00105; AA\_TRANSFERR\_CLASS\_1; 1.  
 DR PFAM: PF00155; aminotran\_1; 1.  
 KW transferase; Aminotransferase; Pyridoxal phosphate; Multigene family.  
 FT BINDING 251 251 PYRIDOXAL PHOSPHATE (BY SIMILARITY).  
 SQ SEQUENCE 405 AA: 44296 MW; A1D4EBF5 CRC32;

QY 2 RYFNOLSTGLDMVGLAAD 19

Search completed: Tue Mar 7 21:41:43 2000  
 Job time : 7 secs.

Query Match 40.0%; Score 62; DB 1; Length 405;  
 Best Local Similarity 44.4%; Pred. No. 5.37e+00;  
 Matches 8; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

Db 152 RYDPAIRGLDFGLLED 169  
 QY 2 RYFNOLSTGLDMVGLAAD 19

RESULT 15  
 ID AATC\_ORYSA STANDARD; PRT; 407 AA.

AC P37833;  
 DT 01-OCT-1994 (Rel. 30, Created)  
 DT 01-OCT-1994 (Rel. 30, Last sequence update)  
 DT 15-JUL-1998 (Rel. 36, Last annotation update)  
 DE ASPARTATE AMINOTRANSFERASE, CYTOPLASMIC (EC 2.6.1.1) (TRANSAMINASE A).  
 OS Oryza sativa (Rice).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC euphyllophytes; Spermatophyta; Magnoliophyta; Liliopsida; Poales;  
 OC Poaceae; Oryza.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CV. NIPPONBARE;  
 RX MEDLINE: 97191542.

RA SONG J., SASAKI T., MINOBE Y.;  
 RT "Characterization and mapping of cDNA encoding aspartate  
 aminotransferase in rice, *Oryza sativa* L.";

RT DNA Res. 3:303-310(1996).  
 CC -!- FUNCTION: IMPORTANT FOR THE METABOLISM OF AMINO ACIDS AND KREBS-  
 CYCLE RELATED ORGANIC ACIDS. IN PLANTS, IT IS INVOLVED IN NITROGEN  
 METABOLISM AND IN ASPECTS OF CARBON AND ENERGY METABOLISM.  
 CC -!- CATALYTIC ACTIVITY: L-ASPARTATE + 2-OXOGLUTARATE = OXALOACETATE +  
 L-GLUTAMATE.  
 CC -!- COFACTOR: PYRIDOXAL PHOSPHATE.  
 CC -!- SUBUNIT: HOMODIMER (BY SIMILARITY).  
 CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).  
 CC -!- SIMILARITY: BELONGS TO CLASS-I OF PYRIDOXAL-PHOSPHATE-DEPENDENT  
 AMINOTRANSFERASES.

CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

CC -----  
 DR EMBL: D14673; BAA03504.1; -  
 DR HSSP: P00508; ITAT.  
 DR PROSITE: PS00105; AA\_TRANSFERR\_CLASS\_1; 1.  
 DR PFAM: PF00155; aminotran\_1; 1.  
 KW transferase; Aminotransferase; Pyridoxal phosphate.  
 FT BINDING 253 253 PYRIDOXAL PHOSPHATE (BY SIMILARITY).  
 SQ SEQUENCE 407 AA: 44507 MW; E5DC8A40 CRC32;

Query Match 40.0%; Score 62; DB 1; Length 407;  
 Best Local Similarity 44.4%; Pred. No. 5.37e+00;  
 Matches 8; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

Db 154 RYDPAIRGLDFGLLED 171  
 QY 2 RYFNOLSTGLDMVGLAAD 19



```

RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 91062362.
RA BOND R.W., WYBORSKI R.J., GOTTLIEB D.I.;
RT "Developmentally regulated expression of an exon containing a stop
RL codon in the gene for glutamic acid decarboxylase."
DR Proc. Natl. Acad. Sci. U.S.A. 87:8771-8775(1990).
DR EMBL: M38350; AAA41185.1; -.
DR PFW: PF00282; pyridoxal_dec; 1.
SQ SEQUENCE 223 AA; 25069 MW; C7162AC1 CRC32;

Query Match
Best Local Similarity 87.1%; Score 135; DB 11; Length 223;
Matches 15; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Db 184 PRFNOLSTGLDMLAGLAW 203
1 PRFNOLSTGLDMLAGLAW 20
1 PRFNOLSTGLDMLAGLAW 20

RESULT 3
ID 008685; PRELIMINARY; PRT; 593 AA.
AC 008685;
DT 01-JUL-1997 (TREMblrel. 04, Created)
DT 01-JUL-1997 (TREMblrel. 04, Last sequence update)
DT 01-NOV-1999 (TREMblrel. 12, Last annotation update)
DE 67KD GLUTAMIC ACID DECARBOXYLASE.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN-BAB/C;
RA AUST G., STEINBRENNER H., THAMM B., ROST A.K., SEISSLER J.;
RL Submitted (Apr-1997) to the EMBL/Genbank/DBJ databases.
CC -1- COFACOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY)
CC -1- SIMILARITY: BELONGS TO GROUP II DECARBOXYLASES (DDC, GAD, HDC AND
CC TYRDC).
DR EMBL: Y12257; CAA72934.1; -.
DR PROSITE: PS00392; DDC_GAD_HDC_YDC; 1.
DR PFW: PF00282; pyridoxal_dec; 1.
KW lase: Decarboxylase; Pyridoxal phosphate.
SQ SEQUENCE 593 AA; 66648 MW; BAFE92E0 CRC32;

Query Match
Best Local Similarity 87.1%; Score 135; DB 11; Length 593;
Matches 15; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Db 184 PRFNOLSTGLDMLAGLAW 203
1 PRFNOLSTGLDMLAGLAW 20
1 PRFNOLSTGLDMLAGLAW 20

RESULT 4
ID 044102; PRELIMINARY; PRT; 370 AA.
AC 044102;
DT 01-JUN-1998 (TREMblrel. 06, Created)
DT 01-JUN-1998 (TREMblrel. 06, Last sequence update)
DT 01-NOV-1999 (TREMblrel. 12, Last annotation update)
DE GLUTAMIC ACID DECARBOXYLASE (FRAGMENT).
GN GAD1.
OS Drosophila pseudoobscura (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
RN [1]
RP SEQUENCE FROM N.A.
RX ZENG L.-W., COMERON J.M., CHEN B., KREITMAN M.;
RL Genetic 0:0-0(1997).
DR EMBL: AF025807; AAB87892.1; -.
DR HSSP: P06543; 100C.
DR FLYBASE: FBgn0023295; Dpse\Gad1.
DR PFW: PF00282; pyridoxal_dec; 2.
SQ SEQUENCE FROM N.A.

```

```

FT NON_TER 1 1
FT NON_TER 370 370
SQ SEQUENCE 370 AA; 41887 MW; A1EB456F CRC32;

Query Match
Best Local Similarity 74.2%; Score 115; DB 5; Length 370;
Matches 11; Conservative 8; Mismatches 1; Indels 0; Gaps 0;

Db 22 PRFNOLSTGLDMLAGLAW 41
1 PRFNOLSTGLDMLAGLAW 20
1 PRFNOLSTGLDMLAGLAW 20

RESULT 5
ID 044103; PRELIMINARY; PRT; 370 AA.
AC 044103;
DT 01-JUN-1998 (TREMblrel. 06, Created)
DT 01-JUN-1998 (TREMblrel. 06, Last sequence update)
DT 01-NOV-1999 (TREMblrel. 12, Last annotation update)
DE GLUTAMIC ACID DECARBOXYLASE (FRAGMENT).
GN GAD1.
OS Drosophila subobscura (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
RN [1]
RP SEQUENCE FROM N.A.
RX ZENG L.-W., COMERON J.M., CHEN B., KREITMAN M.;
RL Genetic 0:0-0(1997).
DR EMBL: AF025808; AAB87893.1; -.
DR HSSP: P06543; 100C.
DR FLYBASE: FBgn0023244; Dsub\Gad1.
DR PFW: PF00282; pyridoxal_dec; 2.
FT NON_TER 1 1
FT NON_TER 370 370
SQ SEQUENCE 370 AA; 41923 MW; D75BDC49 CRC32;

Query Match
Best Local Similarity 74.2%; Score 115; DB 5; Length 370;
Matches 11; Conservative 8; Mismatches 1; Indels 0; Gaps 0;

Db 22 PRFNOLSTGLDMLAGLAW 41
1 PRFNOLSTGLDMLAGLAW 20
1 PRFNOLSTGLDMLAGLAW 20

RESULT 6
ID 09XTP4; PRELIMINARY; PRT; 508 AA.
AC 09XTP4;
DT 01-NOV-1999 (TREMblrel. 12, Created)
DT 01-NOV-1999 (TREMblrel. 12, Last sequence update)
DT 01-NOV-1999 (TREMblrel. 12, Last annotation update)
DE GLUTAMIC ACID DECARBOXYLASE.
GN UNC-25 OR Y37D8A.23.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
OC Rhabditina; Rhabditidae; Rhabditidae; Peloderinae; Caenorhabditis.
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN-BRISTOL;
RX MEDLINE: 99098940.
RX JIN Y., JORGENSEN E., HARTWIG E., HORVITZ H.R.;
RT "The Caenorhabditis elegans gene unc-25 encodes glutamic acid
RL decarboxylase and is required for synaptic transmission but not
RT synaptic development."
RL J. Neurosci. 19:539-548(1999).
RN [2]
RP SEQUENCE FROM N.A.
RX SPECIES=C.elegans;
RA BARLOW K.;
RL Submitted (Oct-1998) to the EMBL/Genbank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.

```

RC SPECIES=C.elegans:  
 RX MEDLINE: 94150718.  
 RA WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,  
 RA BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,  
 RA CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULFON L.,  
 RA GARDNER A., GREEN P., HANKINS T., HILLIER L., JIER M., JOHNSTON L.,  
 RA JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,  
 RA LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,  
 RA PARSONS J., PERCY C., RIKKEN L., ROOPRA A., SAUNDERS D., SHONKKEEN R.,  
 RA SMALLDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,  
 RA THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,  
 RA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.,  
 RA "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.  
 elegans.";  
 RL Nature 368:32-38(1994).  
 DR EMBL: AF109378; AAD19558.1; -;  
 DR EMBL: AL032626; CAA21537.1; -;  
 SQ SEQUENCE 508 AA; 57792 MW; 3A3EF733 CRC32;

Query Match 73.5%; Score 114; DB 5; Length 508;  
 Best Local Similarity 60.0%; Pred. No. 1.26e-10;  
 Matches 12; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

Db 100 PREFNOISGLDVMGEM 119  
 QY 1 PREFNOISGLDVMGEM 20

RESULT 7  
 ID P70713 PRELIMINARY; PRT; 78 AA.  
 AC P70713;  
 DT 01-FEB-1997 (TrEMBLrel. 02, Created)  
 DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)  
 DT 01-NOV-1999 (TrEMBLrel. 10, Last annotation update)  
 DE CYSTEINE SULFINIC ACID DECARBOXYLASE (EC 4.1.1.29)  
 DE (SULFINOLANINE DECARBOXYLASE) (CYSTEINE-SULFINATE DECARBOXYLASE)  
 DE (FRAGMENT).  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-SPRAGUE-DAWLEY; TISSUE-LIVER.  
 RA KRAUSKIN I.U., YU X., SMUTZER G., DOTY R.L.;  
 RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.  
 CC -1- CATALYTIC ACTIVITY: 3-SULFINO-L-ALANINE = HYPOTAURINE + CO(2).  
 CC -1- COFACTOR: PYRIDOXAL-PHOSPHATE.  
 DR EMBL: U74492; AAB18332.1; -;  
 DR PFM: PF00282; pyridoxal\_dec. 1.  
 KW lyase.  
 FT NON\_TER 1 1  
 FT NON\_TER 78 78  
 SQ SEQUENCE 78 AA; 9134 MW; F4808D1F CRC32;

Query Match 51.6%; Score 80; DB 11; Length 78;  
 Best Local Similarity 61.1%; Pred. No. 4.03e-03;  
 Matches 11; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Db 46 PREFNOISGLDVMGEM 63  
 QY 1 PREFNOISGLDVMGEM 18

RESULT 8  
 ID Q9Y602 PRELIMINARY; PRT; 267 AA.  
 AC Q9Y602;  
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)  
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)  
 DT 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)  
 DE CYSTEINE SULFINIC ACID DECARBOXYLASE-RELATED PROTEIN 1.  
 GN CSAD.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

OC Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-BRAIN;  
 RA PRITCHARD J.E., RAMSDEN D.B.;  
 RT "Human cysteine sulfonic acid decarboxylase (CSAD)-related mRNA, 1.";  
 RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF116545; AAD32543.1; -;  
 SQ SEQUENCE 267 AA; 30264 MW; A3475A7D CRC32;

Query Match 51.6%; Score 80; DB 4; Length 267;  
 Best Local Similarity 61.1%; Pred. No. 4.03e-03;  
 Matches 11; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Db 87 PREFNOISGLDVMGEM 104  
 QY 1 PREFNOISGLDVMGEM 18

RESULT 9  
 ID Q64577 PRELIMINARY; PRT; 478 AA.  
 AC Q64577;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)  
 DE CYSTEINE SULFINIC ACID DECARBOXYLASE (EC 4.1.1.29)  
 DE (SULFINOLANINE DECARBOXYLASE) (CYSTEINE-SULFINATE DECARBOXYLASE).  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-SPRAGUE-DAWLEY;  
 RA MEDLINE: 95290499.  
 RA KASAKIA P.J., JERRINS A.A., GOODSPED D.C., STEELE R.D.;  
 RT "Cloning and characterization of rat cysteine sulfonic acid  
 decarboxylase.";  
 RL Biochim. Biophys. Acta 1262:79-82(1995).  
 CC -1- CATALYTIC ACTIVITY: 3-SULFINO-L-ALANINE = HYPOTAURINE + CO(2).  
 CC -1- COFACTOR: PYRIDOXAL-PHOSPHATE.  
 CC -1- COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO GROUP II DECARBOXYLASES (DDC, GAD, HDC AND  
 TYRDC).  
 DR EMBL: M64755; AAC42063.1; -;  
 DR PROSITE: PS00392; DDC\_GAD\_HDC\_YDC; 1.  
 DR PFM: PF00282; pyridoxal\_dec. 1.  
 KW lyase; Decarboxylase; Pyridoxal phosphate.  
 SQ SEQUENCE 478 AA; 53725 MW; 4CAC0093 CRC32;

Query Match 51.6%; Score 80; DB 11; Length 478;  
 Best Local Similarity 61.1%; Pred. No. 4.03e-03;  
 Matches 11; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Db 87 PREFNOISGLDVMGEM 104  
 QY 1 PREFNOISGLDVMGEM 18

RESULT 10  
 ID Q9Y600 PRELIMINARY; PRT; 493 AA.  
 AC Q9Y600;  
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)  
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)  
 DT 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)  
 DE CYSTEINE SULFINIC ACID DECARBOXYLASE-RELATED PROTEIN 3.  
 GN CSAD.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 OC Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-BRAIN;  
 RA PRITCHARD J.E., RAMSDEN D.B.;

RT "Human Cysteine sulfinic acid decarboxylase (CSAD)-related mRNA, 3."  
 RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF116547; AAD32545.1; -  
 SO SEQUENCE 493 AA; 54951 MW; F4852742 CRC32;

Query Match  
 Best Local Similarity 61.1%; Score 80; DB 4; Length 493;  
 Matches 11; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Db 87 PREFNOLSTGLDMVGLAA 104  
 11:1111:111:111:  
 OY 1 PREFNOLSTGLDMVGLAA 18

RESULT 11  
 ID 064611 PRELIMINARY: PRT: 493 AA.  
 AC 064611:  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, last sequence update)  
 DT 01-NOV-1999 (TREMBLrel. 12, last annotation update)  
 DE CYSTEINE SULFINATE DECARBOXYLASE (EC 4.1.1.29)  
 DE (SULFINOALANINE DECARBOXYLASE) (CYSTEINE-SULFINATE DECARBOXYLASE).  
 GN CSD.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE: 96283809.  
 RA REYMOND I., SERGEANT A., TAPPAN M.;  
 RT "Molecular cloning and sequence analysis of the cDNA encoding rat  
 RT liver cysteine sulfinate decarboxylase (CSD)."  
 RL Biochim. Biophys. Acta 1307:152-156(1996).  
 CC -1- SIMILARITY: BELONGS TO GROUP II DECARBOXYLASES (DDC, GAD, HDC AND  
 CC TYRDC).  
 CC EMBL: X94152; CAA63868.1; -  
 DR PROSITE: PS00392; DDC\_GAD\_HDC\_YDC. 1.  
 DR PFAM: PF00282; Pyridoxal-dec. 1.  
 KW Lyase; Decarboxylase; Pyridoxal phosphate.  
 SQ SEQUENCE 493 AA; 55248 MW; D7A6D9A CRC32;

Query Match  
 Best Local Similarity 61.1%; Score 80; DB 11; Length 493;  
 Matches 11; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Db 87 PREFNOLSTGLDMVGLAA 104  
 11:1111:111:111:  
 OY 1 PREFNOLSTGLDMVGLAA 18

RESULT 12  
 ID 017621 PRELIMINARY: PRT: 387 AA.  
 AC 017621:  
 DT 01-JAN-1998 (TREMBLrel. 05, Created)  
 DT 01-JAN-1998 (TREMBLrel. 05, last sequence update)  
 DT 01-JAN-1999 (TREMBLrel. 09, last annotation update)  
 DE C29F7.2 PROTEIN.  
 GN C29F7.2.  
 OS Caenorhabditis elegans.  
 OC Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;  
 OC Rhabditina; Rhabditidae; Rhabditidae; Peloderinae; Caenorhabditis.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MCMURRAY A.;  
 RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE: 94150718.  
 RA WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,  
 RA BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,  
 RA CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,  
 RA GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,

RA JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LAURELLE P.,  
 RA LIGHTNING J., LOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,  
 RA PARNSON J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,  
 RA SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,  
 RA THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,  
 RA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;  
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.  
 RT elegans."  
 RL Nature 368:32-38(1994).  
 DR EMBL: Z92827; CAB07327.1; -  
 SQ SEQUENCE 387 AA; 44178 MW; 7D9B37E1 CRC32;

Query Match  
 Best Local Similarity 47.1%; Score 73; DB 5; Length 387;  
 Matches 8; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Db 305 YFDRSLGLEAKGVKMPW 322  
 11:1111:1:1:  
 OY 3 YFDRSLGLEAKGVKMPW 20

RESULT 13  
 ID 017620 PRELIMINARY: PRT: 394 AA.  
 AC 017620:  
 DT 01-JAN-1998 (TREMBLrel. 05, Created)  
 DT 01-JAN-1998 (TREMBLrel. 05, last sequence update)  
 DT 01-JAN-1999 (TREMBLrel. 09, last annotation update)  
 DE C29F7.1 PROTEIN.  
 GN C29F7.1.  
 OS Caenorhabditis elegans.  
 OC Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;  
 OC Rhabditina; Rhabditidae; Rhabditidae; Peloderinae; Caenorhabditis.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MCMURRAY A.;  
 RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE: 94150718.  
 RA WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,  
 RA BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,  
 RA CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,  
 RA GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,  
 RA JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LAURELLE P.,  
 RA LIGHTNING J., LOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,  
 RA PARNSON J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,  
 RA SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,  
 RA THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,  
 RA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;  
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.  
 RT elegans."  
 RL Nature 368:32-38(1994).  
 DR EMBL: Z92827; CAB07326.1; -  
 SQ SEQUENCE 394 AA; 44297 MW; 35D9F168 CRC32;

Query Match  
 Best Local Similarity 45.8%; Score 71; DB 5; Length 394;  
 Matches 8; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

Db 311 HYFEKLSAGLEKGVKMPW 329  
 11:1111:111:111:  
 OY 2 HYFEKLSAGLEKGVKMPW 20

RESULT 14  
 ID P94758 PRELIMINARY: PRT: 192 AA.  
 AC P94758:  
 DT 01-MAY-1997 (TREMBLrel. 03, Created)  
 DT 01-MAY-1997 (TREMBLrel. 03, last sequence update)  
 DT 01-NOV-1999 (TREMBLrel. 12, last annotation update)  
 DE RIBONUCLEASE (EC 2.7.1.15).  
 OS Escherichia coli.  
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;



OC Escherichia.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-K12:  
 RX MEDLINE: 97251358.  
 RA ITOH T., AIBA H., BABA T., FUJITA K., HAYASHI K., INADA T., ISONO K.,  
 RA KASAI H., KIMURA S., KITAKAWA M., KITAGAWA M., MAKINO K., MIKI T.,  
 RA MIZOBUCHI K., MORI H., MORI T., MOTOMURA K., NAKADE S., NAKAMURA Y.,  
 RA NASHIMOTO H., NISHIO Y., OSHIMA T., SAITO N., SAKPEI G., SEKI Y.,  
 RA SIVASUNDARAM S., TAGAMI H., TAKEDA J., TAKEMOTO K., WADA C.,  
 RA YAMAMOTO Y., HORIUCHI T.;  
 RT "A 450-kb DNA sequence of the Escherichia coli K-12 genome  
 RT corresponding to the 40,1-50.0 min region on the linkage map";  
 RL DNA Res. 3:379-392(1996).  
 DR EMBL: D90848; BAA15968.1;  
 DR PFM: PF00294; pfkb: 1.  
 KW Kinase.  
 SQ SEQUENCE 192 AA; 20544 MW; 1A02381C CRC32;

Query Match 43.9%; Score 68; DB 2; Length 192;  
 Best Local Similarity 45.0%; Pred. No. 8,70e-01;  
 Matches 9; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

Db 16 PALFFRLSTGLARELIVEM 35  
 QY 1 PRYFNQSTGLDMVGLADW 20

RESULT 15  
 ID 052961 PRELIMINARY: PRT: 169 AA.  
 AC 052961.  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)  
 DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)  
 DE ORF14.  
 OS Sinorhizobium meliloti.  
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;  
 OC Rhizobiaceae; Sinorhizobium.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-RU11001;  
 RX MEDLINE: 97474264.  
 RA PLATZER J., STERR W., HAUSMANN M., SCHMITT R.;  
 RT "Three genes of a motility operon and their role in flagellar rotary  
 RT speed variation in Rhizobium meliloti.";  
 RL J. Bacteriol. 179:6391-6399(1997).  
 DR EMBL: L49337; AAB81407.1;  
 SQ SEQUENCE 169 AA; 18440 MW; D1356C2A CRC32;

Query Match 43.2%; Score 67; DB 2; Length 169;  
 Best Local Similarity 72.7%; Pred. No. 1,33e+00;  
 Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db 24 PRYFPDLDTGL 34  
 QY 1 PRYFNQSTGL 11

Search completed: Tue Mar 7 21:43:28 2000  
 Job time : 13 secs.

**THIS PAGE BLANK (USPTO)**

\*\*\*\*\*  
Release 3.1a John F. Collins, Biocomputing Research Unit.  
Copyright (c) 1993-1998 University of Edinburgh, U.K.  
Distribution rights by Oxford Molecular Ltd  
\*\*\*\*\*  
(TM)

\*\*\*\*\*  
Release 3.1a John F. Collins, Biocomputing Research Unit.  
Copyright (c) 1993-1998 University of Edinburgh, U.K.  
Distribution rights by Oxford Molecular Ltd  
\*\*\*\*\*  
Msearch\_pp protein - protein database search, using Smith-Waterman algorithm  
Run on: Tue Mar 7 21:52:24 2000; MasPar time 5.58 Seconds  
169.030 Million cell updates/sec  
Tabular output not generated.

Title: >US-08-981-824-6  
Description: (1-20) from US08981824.pep  
Perfect Score: 155  
Sequence: 1 TYEIAPEVLEVTLEKMR 20

Scoring table: PAM 150  
Gap 15

Searched: 142080 seqs, 47172406 residues

Post-processing: Minimum Match 0%  
Lifting first 45 summaries

Database: par62  
1:pir1 2:pir2 3:pir3 4:pir4

Statistics: Mean 30.538; Variance 48.638; scale 0.628

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	155	100.0	205	2	65 kda glutamate deca	1.21e-17
2	155	100.0	585	1	glutamate decarboxyla	1.21e-17
3	155	100.0	585	1	glutamate decarboxyla	1.21e-17
4	155	100.0	585	1	glutamate decarboxyla	1.21e-17
5	155	100.0	585	2	glutamate decarboxyla	1.21e-17
6	131	84.5	205	2	glutamate decarboxyla	1.21e-17
7	131	84.5	585	2	glutamate decarboxyla	2.07e-12
8	131	84.5	593	2	glutamate decarboxyla	2.07e-12
9	131	84.5	593	2	glutamate decarboxyla	2.07e-12
10	131	84.5	593	2	glutamate decarboxyla	2.07e-12
11	131	84.5	594	2	glutamate decarboxyla	2.07e-12
12	131	84.5	594	2	glutamate decarboxyla	2.07e-12
13	131	84.5	594	2	glutamate decarboxyla	2.07e-12
14	131	84.5	594	2	glutamate decarboxyla	2.07e-12
15	123	79.4	510	1	glutamate decarboxyla	1.02e-10
16	111	71.6	493	2	sulfoalaline decarbox	3.05e-08
17	84	54.2	575	1	glutamate decarboxyla	4.97e-03
18	74	47.7	298	2	hypothetical protein	2.83e-01
19	74	47.7	298	2	conserved hypothetical	8.99e-01
20	71	45.8	436	2	conserved hypothetical	1.31e+00
21	70	45.2	354	2	GTP-binding regulator	1.91e+00
22	69	44.5	487	2	permease 1 - maize	2.77e+00
23	68	43.9	586	2	hypothetical protein	2.77e+00

24	68	43.9	682	1	H69879	ATP-dependent DNA hel	2.77e+00
25	67	43.2	202	1	DEBSSC	succinate dehydrogena	4.01e+00
26	67	43.2	406	2	S07164	hypothetical protein	4.01e+00
27	66	42.6	130	2	E69982	hypothetical protein	5.77e+00
28	65	41.9	429	2	S49595	probable serine prote	8.28e+00
29	65	41.9	477	2	C65096	hypothetical 52.1 kD	8.28e+00
30	64	41.3	324	1	C47691	phospho-N-acetylglut	1.18e+01
31	64	41.3	735	2	T00850	hypothetical protein	1.18e+01
32	64	41.3	823	2	S18968	cytoskeletal precursor	1.18e+01
33	64	41.3	1147	2	JN0599	DNA-binding factor P	1.18e+01
34	64	41.3	1148	2	A49551	replication factor C	1.18e+01
35	64	41.3	1984	2	A4396	p-type cation translo	1.18e+01
36	64	41.3	3412	1	GNWTRB	genome polyprotein -	1.18e+01
37	63	40.6	307	1	DEPG	3-hydroxyacyl-CoA de	1.69e+01
38	63	40.6	314	1	JC4879	3-hydroxyacyl-CoA de	1.69e+01
39	63	40.6	314	1	JC4879	3-hydroxyacyl-CoA de	1.69e+01
40	63	40.6	354	2	S24362	GTP-binding regulator	1.69e+01
41	63	40.6	365	2	T02150	probable (S)-2-hydrox	1.69e+01
42	63	40.6	437	2	A69128	aspartate--cRNA ligas	1.69e+01
43	63	40.6	817	1	KRVGCN	RNA-directed RNA poly	1.69e+01
44	63	40.6	835	2	S75842	nitrogen assimilation	1.69e+01
45	62	40.0	430	2	A49190	corticosteroid-bindin	2.39e+01

## ALIGNMENTS

RESULT 1  
ENTRY 167412 #type fragment  
TITLE 65 kda glutamate decarboxylase, brain - mouse (fragment)  
ORGANISM #formal name Mus musculus; #common name house mouse  
DATE 27-Feb-1997 #sequence; revision 27-Feb-1997 #text; change 30-May-1997

ACCESSIONS 167412  
REFERENCE I53274  
#authors Faulkner-Jones, B.E.; Gram, D.S.; Kun, J.; Harrison, L.C.  
#journal Endocrinology (1993) 133:2962-2972  
#title Localization and quantitation of expression of two glutamate decarboxylase genes in pancreatic beta-cells and other peripheral tissues of mouse and rat.  
#cross-references MIMD:94062679

#accession I67412  
#stratus preliminary; translated from GB/EMBL/DBJ  
##molecule-type mRNA  
##residues 1-205 #label RES  
##cross-references GB:S67454; NID:9456852  
CLASSIFICATION #superfamily human glutamate decarboxylase  
SUMMARY #length 205 #checksum 3167

Query Match 100.0%; Score 155; DB 2; Length 205;  
Best Local Similarity 100.0%; Pred. No. 1.21e-17;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 32 TYEIAPEVLEVTLEKMR 51  
QY 1 TYEIAPEVLEVTLEKMR 20

RESULT 2  
ENTRY JH0423 #type complete  
TITLE glutamate decarboxylase (EC 4.1.1.15) 2 - rat  
ALTERNATE\_NAMES glutamate decarboxylase GAD65; L-glutamate 1-carboxy-lyase  
ORGANISM #formal name Rattus norvegicus; #common name Norway rat  
DATE 31-Mar-1992 #sequence; revision 23-Mar-1995 #text; change 18-Jun-1999

ACCESSIONS JH0423 A60888  
REFERENCE JH0423  
#authors Erlander, M.G.; Tillaakaratne, N.J.K.; Feldblum, S.; Patel, N.; Tobin, A.J.

#journal Neuron (1991) 7:91-100  
#title Two genes encode distinct glutamate decarboxylases.  
#cross-references MIMD:91293943  
#accession JH0423  
#molecule-type mRNA

##residues 1-585 #label ERL  
##cross-references GB:M72422; NID:g204225; PIDN:AAA63488.1; PID:g204226  
#experimental\_source brain  
#note the authors translated the codon GAT for residue 86 as  
428 as Trp  
His, TCA for residue 198 as Ala, and CAG for residue

REFERENCE A60888  
#authors Chang, Y.C.; Gottlieb, D.I.  
#journal J. Neurosci. (1988) 8:2123-2130  
#title Characterization of the proteins purified with monoclonal  
antibodies to glutamic acid decarboxylase.  
#cross-references MUID:88258610  
#accession A60888  
##status preliminary  
##molecule\_type protein  
##residues 'V', 191-194, 'X', 196-203, 'XX', 206-219, 'X', 225-234, 'X',  
'X', 236-247, 'X', 249-266, 'X', 524-537, 539-543, 'V', 547-549,  
'X', 551-553, 'X', 555-558 #label CHA  
#comment This enzyme (GAD) catalyzes the formation of an inhibitory  
neurotransmitter, gamma-aminobutyric acid, from L-glutamic acid;  
it has several isoforms, each encoded by a separate gene.  
CLASSIFICATION #superfamily human glutamate decarboxylase  
KEYWORDS carbon-carbon lyase; carboxy-lyase; phosphoprotein; pyridoxal  
phosphate

FEATURE 396  
#binding-site pyridoxal phosphate (lys) (covalent)  
#status predicted

SUMMARY #length 585 #molecular-weight 65402 #checksum 7756

Query Match 100.0%; Score 155; DB 1; Length 585;  
Best Local Similarity 100.0%; Pred. No. 1,21e-17;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 206 TYEIAPVFLLEYVTLKKMR 225  
|||||  
Oy 1 TYEIAPVFLLEYVTLKKMR 20

RESULT 3  
ENTRY A41292 #type complete  
TITLE glutamate decarboxylase (EC 4.1.1.15) 2 - human  
ALTERNATE\_NAMES glutamate decarboxylase GAD65; L-glutamate 1-carboxy-lyase  
ORGANISM #formal\_name Homo sapiens #common\_name man  
DATE 13-May-1992 #sequence\_revision 23-Mar-1995 #text\_change  
18-Jun-1999

ACCESSIONS A41935; A41292; S30058; B54778  
REFERENCE A41935  
#authors Bu, D.F.; Erlanger, M.G.; Hiltz, B.C.; Tiliakaratne, N.J.K.;  
Kaufman, D.L.; Wagner-McPherson, C.B.; Evans, G.A.; Tobin,  
A.J.  
#journal Proc. Natl. Acad. Sci. U.S.A. (1992) 89:2115-2119  
#title Two human glutamate decarboxylases, 65-kDa GAD and 67-kDa  
GAD, are each encoded by a single gene.  
#cross-references MUID:92196068  
#accession A41935  
##molecule\_type mRNA  
##residues 1-585 #label BU1  
##cross-references GB:M81882; NID:g182933; PIDN:AAA62367.1; PID:g182934  
#experimental\_source brain  
#note #sequence extracted from NCBI backbone (NCBI:88007)

REFERENCE A41292  
#authors Karlsson, A.E.; Hagopian, W.A.; Grubin, C.E.; Dube, S.;  
Disteche, C.M.; Adler, D.A.; Baermeier, H.; Mathewes, S.;  
Grant, F.J.; Foster, D.; Lernermark, A.  
#journal Proc. Natl. Acad. Sci. U.S.A. (1991) 88:8337-8341  
#title Cloning and primary structure of a human islet isoform of  
glutamic acid decarboxylase from chromosome 10.  
#cross-references MUID:92020648  
#accession A41292  
##molecule\_type mRNA  
##residues 1-585 #label KAR  
##cross-references GB:M74826; NID:g182931; PIDN:AAA56491.1; PID:g182932  
#experimental\_source pancreatic islet

REFERENCE S30058  
#authors Mauch, L.; Ahney, C.C.; Berg, H.; Scherbaum, W.A.; Liedvogel,  
B.; Northemann, W.  
#journal Eur. J. Biochem. (1993) 212:597-603  
#title Characterization of a linear epitope within the human  
pancreatic 64-kDa glutamic acid decarboxylase and its  
autoimmune recognition by sera from insulin-dependent  
diabetes mellitus patients.

##cross-references MUID:93185681  
#accession S30058  
##molecule\_type mRNA  
##residues 6-585 #label MAU  
#cross-references EMBL:X69936  
#experimental\_source pancreatic islet

REFERENCE A54778  
#authors Bu, D.F.; Tobin, A.J.  
#journal Genomics (1994) 21:222-228  
#title The exon-intron organization of the genes (GAD1 and GAD2)  
encoding two human glutamate decarboxylases (GAD-67 and  
GAD-65) suggests that they derive from a common ancestral  
GAD.

##cross-references MUID:94375018  
#contents annotation; Intron-exon boundaries  
#comment This enzyme (GAD) catalyzes the formation of an inhibitory  
neurotransmitter, gamma-aminobutyric acid, from L-glutamic acid;  
it has several isoforms, each encoded by a separate gene. GAD has  
also been implicated as an autoantigen in autoimmune disease  
stiff-man syndrome and insulin-dependent diabetes mellitus.

GENETICS  
#gene GDB:GAD2

SUMMARY #length 585 #molecular-weight 65411 #checksum 4799

Query Match 100.0%; Score 155; DB 1; Length 585;  
Best Local Similarity 100.0%; Pred. No. 1,21e-17;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 206 TYEIAPVFLLEYVTLKKMR 225  
|||||  
Oy 1 TYEIAPVFLLEYVTLKKMR 20

RESULT 4  
ENTRY S38533 #type complete  
TITLE glutamate decarboxylase (EC 4.1.1.15) 2 - mouse  
ALTERNATE\_NAMES glutamate decarboxylase GAD65; L-glutamate 1-carboxy-lyase  
ORGANISM #formal\_name Mus musculus #common\_name house mouse  
DATE 20-May-1994 #sequence\_revision 23-Mar-1995 #text\_change  
18-Jun-1999

ACCESSIONS S38533  
REFERENCE S38533  
#authors Lee, D.S.; Tian, J.; Phan, T.; Kaufman, D.L.  
#journal Biochim. Biophys. Acta (1993) 1216:157-160  
#title Cloning and sequence analysis of a murine cDNA encoding  
glutamate decarboxylase (GAD65).  
#cross-references MUID:94032481  
#accession S38533  
##status preliminary  
##molecule\_type mRNA  
##residues 1-585 #label LEF  
##cross-references GB:L16980; NID:g413867; PIDN:AAA93049.1; PID:g413868  
#comment This enzyme (GAD) catalyzes the formation of an inhibitory  
neurotransmitter, gamma-aminobutyric acid, from L-glutamic acid;  
it has several isoforms, each encoded by a separate gene.  
CLASSIFICATION #superfamily human glutamate decarboxylase  
KEYWORDS carbon-carbon lyase; carboxy-lyase; phosphoprotein; pyridoxal



##cross-references GB:M76177; NID:g204227; PIDN:AAA41184.1; PID:g204228  
#accession A43756  
#authors Wyborski, R.J.; Bond, R.W.; Gottlieb, D.I.  
#journal Brain Res. Mol. Brain Res. (1990) 8:193-198  
#title Characterization of a cDNA coding for rat glutamic acid decarboxylase.  
#cross-references NID:91014554  
#accession A43756  
#status preliminary  
#molecule-type mRNA  
#residues 1-593 #label WTB  
##cross-references GB:X57573; NID:g56183; PIDN:CAA40801.1; PID:g56184  
#note the authors translated the codon TGT for residue 412 as Ser and TCT for residue 413 as Cys

REFERENCE JH0195  
#authors Jullien, J.F.; Samama, P.; Mallet, J.  
#journal J. Neurochem. (1990) 54:703-705  
#title Rat brain glutamic acid decarboxylase sequence deduced from a cloned cDNA.  
#cross-references NID:90132703  
#accession JH0195  
#molecule-type mRNA  
#residues 1-102, 'V', 104-283, 'S', 285-286, 'AD', 289-343, 'EA', 346, 'I', 348-351, 'LE', 354-379, 'R', 381-593 #label JUL  
##cross-references GB:X57572; NID:g56185; PIDN:CAA40800.1; PID:g56186  
COMMENT This enzyme (GAD) catalyzes the formation of an inhibitory neurotransmitter, gamma-aminobutyric acid, from L-glutamic acid; it has several isoforms, each encoded by a separate gene.

CLASSIFICATION #superfamily human glutamate decarboxylase  
KEYWORDS carbon-carbon lyase; carboxy-lyase; phosphoprotein; pyridoxal phosphate

FEATURE 404  
#binding-site pyridoxal phosphate (lys) (covalent)  
#status predicted  
#length 593 #molecular-weight 66640 #checksum 3971

SUMMARY  
Query Match 84.5%; Score 131; DB 1; Length 593;  
Best Local Similarity 85.0%; Pred. No. 2.07e-12;  
Matches 17; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 214 TYEIAPFVLMEOITLKMR 233  
|||||||:|:|||||  
Oy 1 TYEIAPFVLMEOITLKMR 20

RESULT 9  
ENTRY S48135 #type complete  
TITLE glutamate decarboxylase (EC 4.1.1.15) - human  
ORGANISM #formal\_name Homo sapiens #common\_name man  
DATE 14-Jul-1995 #sequence\_revision 10-Nov-1995 #text\_change 07-May-1999

ACCESSIONS S48135  
REFERENCE S48135  
#authors Kelly, C.D.; Edwards, Y.; Johnstone, A.P.; Harfst, E.; Nogradi, A.; Nussey, S.S.; Povey, S.; Carter, N.D.; Ann. Hum. Genet. (1992) 56:255-265  
#note Nucleotide sequence and chromosomal assignment of a cDNA encoding the large isoform of human glutamate decarboxylase.  
#cross-references NID:93080286  
#accession S48135  
#molecule-type mRNA  
#residues 1-593 #label KEL  
##cross-references EMBL:222750  
CLASSIFICATION #superfamily human glutamate decarboxylase  
KEYWORDS carbon-carbon lyase; carboxy-lyase  
SUMMARY #length 593 #molecular-weight 66952 #checksum 4836

Query Match 84.5%; Score 131; DB 2; Length 593;  
Best Local Similarity 85.0%; Pred. No. 2.07e-12;  
Matches 17; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 214 TYEIAPFVLMEOITLKMR 233

|||||||:|:|||||  
Oy 1 TYEIAPFVLMEOITLKMR 20

RESULT 10  
ENTRY S51776 #type complete  
TITLE glutamate decarboxylase (EC 4.1.1.15) - human  
ORGANISM #formal\_name Homo sapiens #common\_name man  
DATE 15-Jul-1995 #sequence\_revision 21-Jul-1995 #text\_change 16-Feb-1997

ACCESSIONS S51776  
REFERENCE S51775  
#authors Johnstone, A.  
#submission submitted to the EMBL Data Library, May 1993  
#accession S51776  
#status preliminary  
#molecule-type mRNA  
#residues 1-593 #label JOH  
##cross-references EMBL:222750  
#note this is an unpublished revision to the sequence from reference S48135

CLASSIFICATION #superfamily human glutamate decarboxylase  
KEYWORDS carbon-carbon lyase; carboxy-lyase  
SUMMARY #length 593 #molecular-weight 66946 #checksum 4842

Query Match 84.5%; Score 131; DB 2; Length 593;  
Best Local Similarity 85.0%; Pred. No. 2.07e-12;  
Matches 17; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 214 TYEIAPFVLMEOITLKMR 233  
|||||||:|:|||||  
Oy 1 TYEIAPFVLMEOITLKMR 20

RESULT 11  
ENTRY B41935 #type complete  
TITLE glutamate decarboxylase (EC 4.1.1.15) 1 - human  
ALTERNATE\_NAMES glutamate decarboxylase GAD67; L-glutamate 1-carboxy-lyase  
ORGANISM #formal\_name Homo sapiens #common\_name man  
DATE 31-Dec-1993 #sequence\_revision 23-Mar-1995 #text\_change 18-Jun-1999

ACCESSIONS B41935; JH0805; A61406; PQ0157; PQ0158; B41367; A36463; A54778

REFERENCE A41935  
#authors Bu, D.F.; Erlander, M.G.; Hitz, B.C.; Tiliakaratne, N.J.K.; Kaufman, D.L.; Wagner-McPherson, C.B.; Evans, G.A.; Tobin, A.J.  
Proc. Natl. Acad. Sci. U.S.A. (1992) 89:2115-2119  
#journal Proc. Natl. Acad. Sci. U.S.A. (1992) 89:2115-2119  
#title Two human glutamate decarboxylases, 65-kDa GAD and 67-kDa GAD, are each encoded by a single gene.  
#cross-references NID:92196068  
#accession B41935  
#molecule-type mRNA  
#residues 1-594 #label BUI  
##cross-references GB:M81883; NID:g182935; PIDN:AAA62368.1; PID:g182936  
#experimental\_source pancreatic islet  
#note sequence extracted from NCBI backbone (NCBI:88006)

REFERENCE JH0805  
#authors Kawasaki, E.; Moriyuchi, R.; Watanabe, M.; Satoh, K.; Charles Brunicaardi, F.; Malt, P.C.; Yamaguchi, T.; Mullen, Y.; Akazawa, S.; Miyamoto, T.; Nagataki, S.  
Biochem. Biophys. Res. Commun. (1993) 192:1353-1359  
#journal Cloning and expression of large isoform of glutamic acid decarboxylase from human pancreatic islet.  
#cross-references NID:93282845  
#accession JH0805  
#molecule-type mRNA  
#residues 1-117, 'N', 119-30, 'N', 32-67, 'K', 69-115, 'L', 117-154, 'T', 156-301, 'C', 303-476, 'G', 478-491, 'G', 493-594 #label KAW  
##cross-references GB:S61898; NID:g385310; PIDN:AAA62698.1; PID:g385311  
#experimental\_source pancreatic islet  
REFERENCE JH0806

```

#authors Yamashita, K.; Cram, D.S.; Harrison, L.C.
#journal Biochem. Biophys. Res. Commun. (1993) 192:1347-1352
#title Molecular cloning of full-length glutamic acid decarboxylase
#cross-references M01D:93282844
#accession JH0806
##molecule-type mRNA
##residues 1-67,'K','69-435','L','437-511','S','513-594 ##label YAM
#cross-references GB:561897; NID:g9385450; PIDN:AA826937.1; PID:g9385451
##experimental-source pancreatic islet
REFERENCE
#authors Kelly, C.; Carter, N.D.; Johnstone, A.P.; Nussey, S.S.
#journal Lancet (1991) 338:1468-1469
#title Cloning of large isoform of human brain glutamic acid
#cross-references M01D:92065769
#accession A61406
##molecule-type mRNA
##residues 62-67,'K','69-205','N','207-564','L','566-594 ##label KEL
#experimental-source brain
REFERENCE
#authors Cram, D.S.; Barnett, L.D.; Joseph, J.L.; Harrison, L.C.
#journal Biochem. Biophys. Res. Commun. (1991) 176:1239-1244
#title Cloning and partial nucleotide sequence of human glutamic
#cross-references M01D:91248209
#accession P00157
##molecule-type mRNA
##residues 218-463 ##label CRI
#cross-references GB:M70434
#experimental-source brain
#accession P00158
##molecule-type mRNA
##residues 218-234,'K','236-240','N','242-288','H','290-323','L','325-329,
'D','331-338','L','340-390','S','392-397 ##label C82
#cross-references GB:M70435; NID:g9182941; PIDN:AA52513.1; PID:g9182942
#experimental-source pancreatic islet
REFERENCE
#authors Michelsen, B.K.; Petersen, J.S.; Boel, E.; Møldrup, A.;
Dyberberg, T.; Madsen, O.D.
#journal Proc. Natl. Acad. Sci. U.S.A. (1991) 88:8754-8758
#title Cloning, characterization, and autoimmune recognition of rat
islet glutamic acid decarboxylase in insulin-dependent
diabetes mellitus.
#cross-references M01D:92020930
#accession B41367
##molecule-type mRNA
##residues 317-482,'R','484-594 ##label MIT
REFERENCE
#authors Persson, H.; Peltto-Huikko, M.; Metsis, M.; Soeder, O.; Brene,
S.; Skog, S.; Hoekfelt, T.; Ritzen, E.M.
#journal Mol. Cell. Biol. (1990) 10:4701-4711
#title Expression of the neurotransmitter-synthesizing enzyme
glutamic acid decarboxylase in male germ cells.
#cross-references M01D:9035986
#accession A36463
##molecule-type mRNA
##residues 527-594 ##label PER
#cross-references GB:M55574; NID:g9182929; PIDN:AAA72938.1; PID:g9182930
REFERENCE
#authors Bu, D.F.; Tobin, A.J.
#journal Genomics (1994) 21:222-228
#title The exon-intron organization of the genes (GAD1 and GAD2)
encoding two human glutamate decarboxylases (GAD-67 and
GAD-65) suggests that they derive from a common ancestral
GAD.
#cross-references M01D:94375018
#contents annotation: intron-exon organization
#comment This enzyme (GAD) catalyzes the formation of an inhibitory
neurotransmitter, gamma-aminobutyric acid, from L-glutamic acid.
It has several isoforms, each encoded by a separate gene. GAD has
also been implicated as an autoantigen in autoimmune disease
stiff-man syndrome and insulin-dependent diabetes mellitus.

```

```

GENETICS
#gene GDB:GAD1, GAD
#cross-references GDB:119244; OMIM:266100
#map_position 2q31-2q31
CLASSIFICATION
#superfamily human glutamate decarboxylase
KEYWORDS
#alternative splicing; carbon-carbon lyase; carboxy-lyase;
phosphoprotein; pyridoxal phosphate
FEATURE
405 #binding_site pyridoxal phosphate (Lys) (covalent)
#status predicted
SUMMARY
#length 594 #molecular-weight 66924 #checksum 6189
Query Match 84.5%; Score 131; DB 1; Length 594;
Best Local Similarity 85.0%; Pred. No. 2.07e-12;
Matches 17; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
Db 215 TVEIAPFVLMEOITLKKMR 234
|||||:|||||:|:|||||
QY 1 TVEIAPFVLELYTLKKMR 20

RESULT 12
ENTRY S51775 #type complete
TITLE glutamate decarboxylase (EC 4.1.1.15) - human
ORANISM #formal_name Homo sapiens #common_name man
DATE 15-Jul-1995 #sequence_revision 21-Jul-1995 #text_change
22-Jun-1999
ACCESSIONS
S51775
S51775
REFERENCE
#authors Johnstone, A.
#submission submitted to the EMBL Data Library, May 1993
#accession S51775
#status preliminary
##molecule-type mRNA
##residues 1-594 ##label JOH
#cross-references EMBL:Z22750; NID:g9298098; PIDN:CA80435.1;
PID:g9298099
CLASSIFICATION
#superfamily human glutamate decarboxylase
KEYWORDS
#carbon-carbon lyase; carboxy-lyase
SUMMARY
#length 594 #molecular-weight 66973 #checksum 6437
Query Match 84.5%; Score 131; DB 2; Length 594;
Best Local Similarity 85.0%; Pred. No. 2.07e-12;
Matches 17; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
Db 215 TVEIAPFVLMEOITLKKMR 234
|||||:|||||:|:|||||
QY 1 TVEIAPFVLELYTLKKMR 20

RESULT 13
ENTRY A46758 #type complete
TITLE glutamate decarboxylase (EC 4.1.1.15) 1 - cat
ALTERNATE_NAMES
#formal_name Feliis silvestris catus #common_name domestic cat
ORANISM
DATE 31-Dec-1993 #sequence_revision 23-Mar-1995 #text_change
18-Jun-1999
ACCESSIONS
A46758; A45671
A46758
REFERENCE
#authors Kobayashi, Y.; Kaufman, D.L.; Tobin, A.J.
#submission submitted to GenBank, September 1989
#accession A46758
##molecule-type mRNA
##residues 1-594 ##label KOB
#cross-references GB:M18629; NID:g9163858; PIDN:AAA51430.1; PID:g9163859
REFERENCE
#authors Kobayashi, Y.; Kaufman, D.L.; Tobin, A.J.
#journal J. Neurosci. (1987) 7:2768-2772
#title Glutamic acid decarboxylase cDNA: nucleotide sequence
encoding an enzymatically active fusion protein.
#cross-references M01D:87310623
#accession A45671
##molecule-type mRNA

```

```
##residues 1-558,'RGRPRFGMSSTQLHSPILTSSRR' ##label KO2
#note This sequence has been revised in reference A6758
COMMENT This enzyme (GAD) catalyzes the formation of an inhibitory
neurotransmitter, gamma-aminobutyric acid, from L-glutamic acid;
it has several isoforms, each encoded by a separate gene.
GENETICS
#gene GAD1
CLASSIFICATION #superfamily human glutamate decarboxylase
KEYWORDS carbon-carbon lyase; carboxy-lyase; phosphoprotein; pyridoxal
phosphate
FEATURE
405 #binding_site pyridoxal phosphate (lys) (covalent)
#status predicted
SUMMARY #length 594 #molecular-weight 66824 #checksum 5630
Query Match 84.5%; Score 131; DB 1; Length 594;
Best Local Similarity 85.0%; Pred. No. 2,07e-12;
Matches 17; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
Db 215 TYEIAPVFLMEQITLTKRM 234
OY 1 TYEIAPVFLLEVYTLTKRM 20
RESULT 14
ENTRY JC4065 #type complete
TITLE glutamate decarboxylase (EC 4.1.1.15) 67K chain - pig
ORGANISM #formal_name Sus scrofa domestica #common_name domestic pig
DATE 30-Jun-1995 #sequence_revision 14-Jul-1995 #text_change
22-Jun-1999
ACCESSIONS JC4065
REFERENCE JC4064
#authors Suzuki, R.; Asami, N.; Amann, E.; Wagatsuma, M.
#journal Gene (1995) 152:257-260
#title Sequences of two porcine glutamic acid decarboxylases (65-and
67-kDa GAD).
#cross-references MUID:95137399
#accession JC4065
#molecule_type mRNA
#residues 1-594 #label SUZ
##cross-references DDBJ:D31849; NID:g790966; PIDN:BAA06636.1;
PID:d1007208; PID:g790967
#experimental_source brain
COMMENT This enzyme catalyzes the conversion of glutamic acid into
gamma-amino butyric acid.
CLASSIFICATION #superfamily human glutamate decarboxylase
KEYWORDS carbon-carbon lyase; carboxy-lyase
FEATURE
402-405 #domain DOPA decarboxylase binding #status predicted
#label BIN
SUMMARY #length 594 #molecular-weight 66894 #checksum 5491
Query Match 84.5%; Score 131; DB 2; Length 594;
Best Local Similarity 85.0%; Pred. No. 2,07e-12;
Matches 17; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
Db 215 TYEIAPVFLMEQITLTKRM 234
OY 1 TYEIAPVFLLEVYTLTKRM 20
RESULT 15
ENTRY A30999 #type complete
TITLE glutamate decarboxylase (EC 4.1.1.15) Cl - fruit fly
ALTERNATE_NAMES (Drosophila melanogaster)
ORGANISM L-glutamate 1-carboxy-lyase
DATE #formal_name Drosophila melanogaster
26-Oct-1989 #sequence_revision 23-Mar-1995 #text_change
18-Jun-1999
ACCESSIONS JH0192; PS0301; A30999
REFERENCE JH0192
#authors Jackson, F.R.; Newby, L.M.; Kulkarni, S.J.
#journal J. Neurochem. (1990) 54:1068-1078
```

```
#title Drosophila GABAergic systems: sequence and expression of
glutamic acid decarboxylase.
#cross-references MUID:90155291
#accession JH0192
#molecule_type mRNA
#residues 1-510 #label JAC
##cross-references GB:X76198; NID:g433082; PIDN:CAAS3791.1; PID:g433083
#accession PS0301
#molecule_type mRNA
#residues 156-200,'F',202-300,'K',302-384,'L',386-510 ##label JA2
COMMENT This enzyme (GAD) catalyzes the formation of an inhibitory
neurotransmitter, gamma-aminobutyric acid, from L-glutamic acid;
it has several isoforms, each encoded by a separate gene.
GENETICS
#gene FlyBase:Gad1
#cross-references FlyBase:FBgn0004516
CLASSIFICATION #superfamily human glutamate decarboxylase
KEYWORDS carbon-carbon lyase; carboxy-lyase; phosphoprotein; pyridoxal
phosphate
FEATURE
322 #binding_site pyridoxal phosphate (lys) (covalent)
#status predicted
SUMMARY #length 510 #molecular-weight 57758 #checksum 3194
Query Match 79.4%; Score 123; DB 1; Length 510;
Best Local Similarity 75.0%; Pred. No. 1,02e-10;
Matches 15; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
Db 132 TYEIAPVFLMEQITLTKRM 151
OY 1 TYEIAPVFLLEVYTLTKRM 20
```

Search completed: Tue Mar 7 21:52:32 2000  
job time : 8 secs.





Db 206 TYEIAPVFVLEVTLLKMR 225  
 ||||||||||||||||  
 QY 1 TYEIAPVFVLEVTLLKMR 20

RESULT 2  
 ID DCE2.PIG STANDARD: PRT: 585 AA.

AC P48321;  
 DT 01-FEB-1996 (Rel. 33, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 01-FEB-1996 (Rel. 33, Last annotation update)  
 DE GLUTAMATE DECARBOXYLASE, 65 KD ISOFORM (EC 4.1.1.15) (GAD-65)  
 GN GAD2 OR GAD65.  
 OS Sus scrofa (Pig).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 RN Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

RP SEQUENCE FROM N.A.  
 RC TISSUE-BRAIN;  
 RX MEDLINE: 95137399.

RA SUZUKI R., ASAMI N., AMANN E., WAGATSUMA M.;

RT "Sequences of two porcine glutamic acid decarboxylases (65- and 67-kDa GAD).";

RL Gene 152:257-260(1995).

CC -1- FUNCTION: CATALYZES THE PRODUCTION OF GABA.

CC -1- CATALYTIC ACTIVITY: L-GLUTAMATE = 4-AMINOBUTANOATE + CO(2).

CC -1- COFACTOR: PYRIDOXAL PHOSPHATE.

CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).

CC -1- SIMILARITY: BELONGS TO GROUP II DECARBOXYLASES (DDC, GAD, HDC AND TYROC).

-----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 -----

CC EMBL: D31848; BAA0635.1; -

DR PROSITE: PS00392; DDC\_GAD\_HDC\_YDC; 1.

DR PFAM: PF00282; pyridoxal\_dec; 1.

KW Neurotransmitter biosynthesis; Lyase; Decarboxylase;

KW Pyridoxal phosphate; Multigene family.

FT BINDING 396 PYRIDOXAL PHOSPHATE (POTENTIAL).

SEQUENCE 585 AA: 65388 MW; F3E9BD88 CRC32;

Query Match 100.0%; Score 155; DB 1; Length 585;

Best Local Similarity 100.0%; Pred. No. 6,44e-21;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 206 TYEIAPVFVLEVTLLKMR 225  
 ||||||||||||||||

QY 1 TYEIAPVFVLEVTLLKMR 20

RESULT 3  
 ID DCE2.HUMAN STANDARD: PRT: 585 AA.

AC 005329;  
 DT 01-FEB-1996 (Rel. 33, Created)

DT 01-FEB-1996 (Rel. 33, Last sequence update)

DT 01-FEB-1996 (Rel. 33, Last annotation update)

DE GLUTAMATE DECARBOXYLASE, 65 KD ISOFORM (EC 4.1.1.15) (GAD-65)

DE (65 KD GLUTAMIC ACID DECARBOXYLASE).

GN GAD2 OR GAD65.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

OC Eutheria; Primates; Catarrhini; Homiidae; Homo..

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE: 92196068.

BU D.-F., ERLANDER M.G., HITZ B.C., TILLAKARATNE N.J., KAUFMAN D.L.,

RA WAGNER-MCPHERSON C.B., EVANS G.A., TOBIN A.J.;  
 RT "Two human glutamate decarboxylases, 65-kDa GAD and 67-kDa GAD, are  
 RT each encoded by a single gene."  
 RL Proc. Natl. Acad. Sci. U.S.A. 89:2115-2119(1992).

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE: 94375018.

RA BU D.-F., TOBIN A.J.;

RT "The exon-intron organization of the genes (GAD1 and GAD2) encoding  
 RT two human glutamate decarboxylases (GAD67 and GAD65) suggests that  
 RT they derive from a common ancestral GAD.";

RL Genomics 21:222-228(1994).

RN [3]

RP SEQUENCE FROM N.A.

RC TISSUE-PANCREATIC ISLETS;

RX MEDLINE: 92020848.

RA KARLSEN A.E., HAGOPIN W.A., GRUBIN C.E., DUBE S., DISTECHE C.M.,

RA ADLER D.A., BARMEIER H., MATHIENS S., GRANT F.J., FOSTER D.,

RA LERNMARK A.;

RT "Cloning and primary structure of a human islet isoform of glutamic  
 RT acid decarboxylase from chromosome 10.";

RL Proc. Natl. Acad. Sci. U.S.A. 88:8337-8341(1991).

RN [4]

RP SEQUENCE OF 6-585 FROM N.A.

RC TISSUE-PANCREAS;

RX MEDLINE: 93185681.

RA MAUCH L., ABNEY C.C., BERG H., SCHERBAUM W.A., LIEBVOGEL B.,

RA NORTHEMANN W.;

RT "Characterization of a linear epitope within the human pancreatic  
 RT 64-kDa glutamic acid decarboxylase and its autoimmune recognition by  
 RT sera from insulin-dependent diabetes mellitus patients.";

RL Eur. J. Biochem. 212:597-603(1993).

CC -1- FUNCTION: CATALYZES THE PRODUCTION OF GABA.

CC -1- CATALYTIC ACTIVITY: L-GLUTAMATE = 4-AMINOBUTANOATE + CO(2).

CC -1- COFACTOR: PYRIDOXAL PHOSPHATE.

CC -1- SUBUNIT: PYRIDOXAL PHOSPHATE.

CC -1- SIMILARITY: LOCAL TO DOPA DECARBOXYLASE, AND TO PLP-TYPE HISTIDINE  
 CC DECARBOXYLASE.

-----

CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 -----

CC EMBL: M81882; AAA62367.1; -

DR EMBL: M74826; AAA58491.1; -

DR EMBL: X69936; CAA49554.1; ALT\_INIT.

DR EMBL: M70435; AAA52513.1; -

DR PIR: A41292; A41292.

DR PIR: P00158; P00158.

DR TM: 138275; -

DR PROSITE: PS00392; DDC\_GAD\_HDC\_YDC; 1.

DR PFAM: PF00282; pyridoxal\_dec; 1.

KW Neurotransmitter biosynthesis; Lyase; Decarboxylase;

KW Pyridoxal phosphate; Multigene family.

FT BINDING 396 PYRIDOXAL PHOSPHATE (BY SIMILARITY).

SEQUENCE 585 AA: 65411 MW; 8AD62B62 CRC32;

Query Match 100.0%; Score 155; DB 1; Length 585;

Best Local Similarity 100.0%; Pred. No. 6,44e-21;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 206 TYEIAPVFVLEVTLLKMR 225  
 ||||||||||||||||

QY 1 TYEIAPVFVLEVTLLKMR 20

RESULT 4  
 ID DCE2.MOUSE STANDARD: PRT: 585 AA.

AC P48320; O35519;

DT 01-FEB-1996 (Rel. 33, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 15-JUL-1998 (Rel. 36, Last annotation update)  
 DE GLUTAMATE DECARBOXYLASE, 65 KD ISOFORM (EC 4.1.1.15) (GAD-65)  
 DE (65 KD GLUTAMIC ACID DECARBOXYLASE).  
 GN GAD2 OR GAD65.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6; TISSUE=BRAIN;  
 RX MEDLINE: 94032481.  
 RA LEE D.S., TIAN J., PHAN T., KAUFMAN D.L.;  
 RT "Cloning and sequence analysis of a murine cDNA encoding glutamate  
 RT decarboxylase (GAD65)."  
 RL Biochim. Biophys. Acta 1216:157-160(1993).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6; TISSUE=BRAIN;  
 RX MEDLINE: 97115675.  
 RA ASADA H., KAWAMURA Y., MARYAMA K., KUME H., DING R.G., JI F.Y.,  
 RA KAWABARA N., KUZUME H., SANBO M., YAGI T., OBATA K.;  
 RT "Mice lacking the 65 kDa isoform of glutamic acid decarboxylase  
 RT (GAD65) maintain normal levels of GAD67 and GABA in their brains but  
 RT are susceptible to seizures."  
 RL Biochem. Biophys. Res. Commun. 229:891-895(1996).  
 RN [3]  
 RP SEQUENCE OF 175-379 FROM N.A.  
 RC TISSUE=BRAIN;  
 RX MEDLINE: 94062679.  
 RA FAULKNER-JONES B.E., CRAM D.S., KUN J., HARRISON L.C.;  
 RT "Localization and quantitation of expression of two glutamate  
 RT decarboxylase genes in pancreatic beta-cells and other peripheral  
 RT tissues of mouse and rat."  
 RL Endocrinology 133:2962-2972(1993).  
 CC -1- FUNCTION: CATALYZES THE PRODUCTION OF GABA.  
 CC -1- CATALYTIC ACTIVITY: L-GLUTAMATE = 4-AMINOBUTANOATE + CO(2).  
 CC -1- COFACTOR: PYRIDOXAL PHOSPHATE.  
 CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).  
 CC -1- SIMILARITY: LOCAL TO DOPA DECARBOXYLASE, AND TO PLP-TYPE HISTIDINE  
 CC DECARBOXYLASE.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL: L16980; AAA93049.1; -;  
 DR EMBL: DA2051; BAA22893.1; -;  
 DR EMBL: S67454; CAB32805.1; -;  
 DR MGD: MGI:95634; GAD2.  
 DR PROSITE: PS00392; DDC\_GAD\_HDC\_YDC; 1.  
 DR PFM: PFM00282; pyridoxal\_dec; 1.  
 KW Neurotransmitter biosynthesis; Lyase; Decarboxylase;  
 KW Pyridoxal phosphate; Multigene family;  
 FT BINDING 396  
 FT CONFLICT 359  
 FT CONFLICT 319  
 FT CONFLICT 325  
 FT CONFLICT 499  
 SO SEQUENCE 585 AA; 65224 MM; 98B5C088 CRC32;  
 Query Match 100.0%; Score 155; DB 1; Length 585;  
 Best Local Similarity 100.0%; Pred. No. 6,44e-21;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 5  
 ID DCEL\_MOUSE STANDARD: PRT: 593 AA.  
 AC P48318;  
 DT 01-FEB-1996 (Rel. 33, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 01-FEB-1996 (Rel. 33, Last annotation update)  
 DE GLUTAMATE DECARBOXYLASE, 67 KD ISOFORM (EC 4.1.1.15) (GAD-67)  
 DE (67 KD GLUTAMIC ACID DECARBOXYLASE).  
 GN GAD1 OR GAD67.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=BRAIN;  
 RA KARAROVA Z., SZABO G., MUGNAINI E., GREENSPAN R.;  
 RT "Molecular identification of the 62 kd form of glutamic acid  
 RT decarboxylase from the mouse."  
 RL Eur. J. Neurosci. 2:190-202(1990).  
 RN [2]  
 RP SEQUENCE OF 198-403 FROM N.A.  
 RC TISSUE=BRAIN;  
 RX MEDLINE: 94062679.  
 RA FAULKNER-JONES B.E., CRAM D.S., KUN J., HARRISON L.C.;  
 RT "Localization and quantitation of expression of two glutamate  
 RT decarboxylase genes in pancreatic beta-cells and other peripheral  
 RT tissues of mouse and rat."  
 RL Endocrinology 133:2962-2972(1993).  
 CC -1- FUNCTION: CATALYZES THE PRODUCTION OF GABA.  
 CC -1- CATALYTIC ACTIVITY: L-GLUTAMATE = 4-AMINOBUTANOATE + CO(2).  
 CC -1- COFACTOR: PYRIDOXAL PHOSPHATE.  
 CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO GROUP II DECARBOXYLASES (DDC, GAD, HDC AND  
 CC TYRDC).  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL: 249976; CA90077.1; -;  
 DR EMBL: S67453; CAB32805.1; -;  
 DR MGD: MGI:95632; GAD1.  
 DR PROSITE: PS00392; DDC\_GAD\_HDC\_YDC; 1.  
 DR PFM: PFM00282; pyridoxal\_dec; 1.  
 KW Neurotransmitter biosynthesis; Lyase; Decarboxylase;  
 KW Pyridoxal phosphate; Multigene family;  
 FT BINDING 404  
 FT CONFLICT 234  
 FT CONFLICT 258  
 FT CONFLICT 360  
 SO SEQUENCE 593 AA; 66584 MM; 63BC57AA CRC32;  
 Query Match 84.5%; Score 131; DB 1; Length 593;  
 Best Local Similarity 85.0%; Pred. No. 6,98e-15;  
 Matches 17; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 214 TYEIAPVFLVEYTLTKMR 233  
 1 TYEIAPVFLVEYTLTKMR 20

RESULT 6  
 ID DCEL\_RAT STANDARD: PRT: 593 AA.  
 AC P18088;  
 DT 01-NOV-1990 (Rel. 16, Created)  
 DT 01-NOV-1990 (Rel. 16, Last sequence update)  
 DT 01-FEB-1996 (Rel. 33, Last annotation update)

```

DE  GLUTAMATE DECARBOXYLASE, 67 KD ISOFORM (EC 4.1.1.15) (GAD-67)
DE  (67 KD GLUTAMIC ACID DECARBOXYLASE).
GN  GAD1 OR GAD67.
OS  Rattus norvegicus (Rat).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC  Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN  [1]
RX  SEQUENCE FROM N.A.
RX  MEDLINE: 91014554.
RA  WYBORSKI R.J., BOND R.W., GOTTLIEB D.I.;
RA  "Characterization of a cDNA coding for rat glutamic acid
RT  decarboxylase."
RT  Brain Res. Mol. Brain Res. 8:193-198(1990).
RN  [2]
RX  SEQUENCE FROM N.A.
RX  MEDLINE: 90132703.
RA  JULIEN J.F., SAMAMA P., MALLET J.;
RA  "Rat brain glutamic acid decarboxylase sequence deduced from a cloned
RT  cDNA."
RT  J. Neurochem. 54:703-705(1990).
RN  [3]
RX  SEQUENCE FROM N.A.
RX  MEDLINE: 92020930.
RA  MICHELSEN B.K., PETERSEN J.S., BOEL E., MOLDROP A., DYRBERG T.,
RA  MADSEN O.D.;
RA  "Cloning, characterization, and autoimmune recognition of rat islet
RT  glutamic acid decarboxylase in insulin-dependent diabetes mellitus."
RT  Proc. Natl. Acad. Sci. U.S.A. 88:8754-8758(1991).
CC  -1- FUNCTION: CATALYZES THE PRODUCTION OF GABA.
CC  -1- CATALYTIC ACTIVITY: L-GLUTAMATE = 4-AMINOBUTANOATE + CO(2).
CC  -1- COFACTOR: PYRIDOXAL PHOSPHATE.
CC  -1- SUBUNIT: HOMODIMER.
CC  -1- SIMILARITY: BELONGS TO GROUP II DECARBOXYLASES (DDC, GAD, HDC AND
CC  TYRDC).
CC  -----
CC  This SWISS-PROT entry is copyright. It is produced through a collaboration
CC  between the Swiss Institute of Bioinformatics and the EMBL outstation-
CC  the European Bioinformatics Institute. There are no restrictions on its
CC  use by non-profit institutions as long as its content is in no way
CC  modified and this statement is not removed. Usage by and for commercial
CC  entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC  or send an email to license@sib-sib.ch).
CC  -----
DR  EMBL: M34445; AAC2037.1; -
DR  EMBL: X57572; CAA40800.1; -
DR  EMBL: X57573; CAA40801.1; -
DR  EMBL: M76177; AAA41184.1; -
DR  PIR: A43756; A43756.
DR  PIR: A43756; A43756.
DR  PROSITE: PS00392; DDC_GAD_HDC_YDC; 1.
DR  PFM: PFM0282; pyridoxal_dec; 1.
KW  Neurotransmitter biosynthesis; Lyase; Decarboxylase;
KW  Pyridoxal phosphate; Multigene family.
FT  BINDING 404 404 PYRIDOXAL PHOSPHATE (POTENTIAL).
FT  CONFLICT 103 103 L -> V (IN REF. 2).
FT  CONFLICT 284 284 F -> S (IN REF. 2).
FT  CONFLICT 287 288 EH -> AD (IN REF. 2).
FT  CONFLICT 344 345 AG -> EA (IN REF. 2).
FT  CONFLICT 347 347 T -> I (IN REF. 2).
FT  CONFLICT 352 353 FD -> LE (IN REF. 2).
FT  CONFLICT 380 380 L -> R (IN REF. 2).
SQ  SEQUENCE 593 AA; 66640 MW; 5A0B67C0 CRC32;

```

```

ID  DCEL_PIG STANDARD; PRT: 594 AA.
AC  P48319;
DT  01-FEB-1996 (Rel. 33, Created)
DT  01-FEB-1996 (Rel. 33, Last sequence update)
DT  01-FEB-1996 (Rel. 33, Last annotation update)
DE  GLUTAMATE DECARBOXYLASE, 67 KD ISOFORM (EC 4.1.1.15) (GAD-67)
DE  (67 KD GLUTAMIC ACID DECARBOXYLASE).
GN  GAD1 OR GAD67.
OS  Sus scrofa (Pig).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC  Eutheria; Cetartiodactyla; Suidae; Suidae; Sus.
RN  [1]
RX  SEQUENCE FROM N.A.
RX  TISSUE-BRAIN;
RX  MEDLINE: 95137399.
RA  SUZUKI R., ASAMI N., AMANN E., WAGATSUMA M.;
RA  "Sequences of two porcine glutamic acid decarboxylases (65- and
RT  67-kDa GAD)."
RT  Gene 152:257-260(1995).
CC  -1- FUNCTION: CATALYZES THE PRODUCTION OF GABA.
CC  -1- CATALYTIC ACTIVITY: L-GLUTAMATE = 4-AMINOBUTANOATE + CO(2).
CC  -1- COFACTOR: PYRIDOXAL PHOSPHATE.
CC  -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC  -1- SIMILARITY: BELONGS TO GROUP II DECARBOXYLASES (DDC, GAD, HDC AND
CC  TYRDC).
CC  -----
CC  This SWISS-PROT entry is copyright. It is produced through a collaboration
CC  between the Swiss Institute of Bioinformatics and the EMBL outstation-
CC  the European Bioinformatics Institute. There are no restrictions on its
CC  use by non-profit institutions as long as its content is in no way
CC  modified and this statement is not removed. Usage by and for commercial
CC  entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC  or send an email to license@sib-sib.ch).
CC  -----
DR  EMBL: D31849; BAA0636.1; -
DR  PROSITE: PS00392; DDC_GAD_HDC_YDC; 1.
DR  PFM: PFM0282; pyridoxal_dec; 1.
KW  Neurotransmitter biosynthesis; Lyase; Decarboxylase;
KW  Pyridoxal phosphate; Multigene family.
FT  BINDING 405 405 PYRIDOXAL PHOSPHATE (POTENTIAL).
FT  BINDING 405 405 PYRIDOXAL PHOSPHATE (POTENTIAL).
SQ  SEQUENCE 594 AA; 66894 MW; 69D6C79C CRC32;

```

Query Match 84.5%; Score 131; DB 1; Length 594;  
Best Local Similarity 85.0%; Pred. No. 6,98e-15;  
Matches 17; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

```

Db  215 TYEIAPVFVLEMTLTKMR 234
QY  1 TYEIAPVFVLEMTLTKMR 20

```

RESULT 8  
DCEL\_HUMAN STANDARD; PRT: 594 AA.  
AC O99259;  
DT 01-FEB-1996 (Rel. 33, Created)  
DT 01-FEB-1996 (Rel. 33, Last sequence update)  
DT 01-OCT-1996 (Rel. 34, Last annotation update)  
DE GLUTAMATE DECARBOXYLASE, 67 KD ISOFORM (EC 4.1.1.15) (GAD-67)  
DE (67 KD GLUTAMIC ACID DECARBOXYLASE).  
GN GAD1 OR GAD.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
OC Eutheria; Primates; Catarrhini; Homidae; Homo.  
RN [1]  
RX SEQUENCE FROM N.A.  
RX TISSUE-BRAIN;  
RX MEDLINE: 92196068.  
RA BU D.-F., ERLANDER M.G., HITZ B.C., TILAKARATNE N.J., KAUFMAN D.L.,  
RA WAGNER-MCPHERSON C.B., EVANS G.A., TOBIN A.J.;  
RA "Two human glutamate decarboxylases, 65-kDa GAD and 67-kDa GAD, are  
RT each encoded by a single gene."  
RT Proc. Natl. Acad. Sci. U.S.A. 89:2115-2119(1992).  
RN [2]



```

CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M18629; AAA51430.1; -.
DR PIR; A45671; A45671.
DR PIR; A46758; A46758.
DR PROSITE; PS00392; DDC_GAD_HDC_YDC; 1.
DR PFAM; PF00282; pyridoxal_dec; 1.
DR Neurotransmitter biosynthesis; Lyase; Decarboxylase;
KW Pyridoxal phosphate; Multigene family.
FT BINDING 405 405
SQ SEQUENCE 594 AA; 66824 MW; 3EC20778 CRC32;

Query Match 84.5%; Score 131; DB 1; Length 594;
Best Local Similarity 85.0%; Pred. No. 6.98e-15;
Matches 17; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 215 TYEAPVLEVTITLKKMR 234
1 TYEAPVLEVTITLKKMR 20

RESULT 10
ID DCE.DROME STANDARD; PRT; 510 AA.
AC P20228;
DI 01-FEB-1991 (Rel. 17, Created)
DI 01-FEB-1991 (Rel. 17, Last sequence update)
DI 01-NOV-1995 (Rel. 32, Last annotation update)
DE GLUTAMATE DECARBOXYLASE (EC 4.1.1.15) (GAD).
OS GAD OR GLB.
SN Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 90155291.
RA JACKSON F.R., NEMBY L.M., KULKARNI S.J.;
RT "Drosophila GABAergic systems: sequence and expression of glutamic
RT acid decarboxylase."
RL J. Neurochem. 54:1068-1078(1990).
CC -1- FUNCTION: CATALYZES THE PRODUCTION OF GABA.
CC -1- CATALYTIC ACTIVITY: L-GLUTAMATE = 4-AMINOBTANONATE + CO(2).
CC -1- COFACTOR: PYRIDOXAL PHOSPHATE.
CC -1- SUBUNIT: HOMODIMER.
CC -1- SIMILARITY: BELONGS TO GROUP II DECARBOXYLASES (DDC, GAD, HDC AND
CC TYRDC).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X76198; CA853791.1; -.
DR PIR; A30999; A30999.
DR PIR; JH0192; JH0192.
DR FLYBASE; FBgn0004516; Gad1.
DR PROSITE; PS00392; DDC_GAD_HDC_YDC; 1.
DR PFAM; PF00282; pyridoxal_dec; 1.
DR Neurotransmitter biosynthesis; Lyase; Decarboxylase;
KW Pyridoxal phosphate.
FT BINDING 322 322
SQ SEQUENCE 510 AA; 57758 MW; 97C7A8F1 CRC32;

Query Match 79.4%; Score 123; DB 1; Length 510;
Best Local Similarity 75.0%; Pred. No. 6.19e-13;
Matches 15; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Db 132 TYEAPVLEVTITLKKMR 151
1 TYEAPVLEVTITLKKMR 20

```

```

RESULT 11
ID YC34_HELPY STANDARD; PRT; 298 AA.
AC 025832;
DI 15-JUL-1999 (Rel. 38, Created)
DI 15-JUL-1999 (Rel. 38, Last sequence update)
DI 15-JUL-1999 (Rel. 38, Last annotation update)
DE HYPOTHETICAL PROTEIN HP1234.
OS HP1234.
SN Helicobacter pylori (Campylobacter pylori).
OC Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
OC Helicobacter.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-26695 / ATCC 700392;
RX MEDLINE; 97394467.
RA TOMB J.-F., WHITE O., KERLAVAGE A.R., CLAYTON R.A., SUTTON G.G.,
RA FLEISCHMANN R.D., KETCHUM K.A., KLENK H.-P., GILL S., DOUGHERTY B.A.,
RA NELSON K., QUACKENBUSH J., ZHOU L., KIRKNESS E.F., PETERSON S.,
RA LOFTUS B., RICHARDSON D., DODSON R., KHALAK H.G., GLODER A.,
RA MCKENNEY K., FITZGERALD L.M., LEE N., ADAMS M.D., HICKEY E.K.,
RA BERG D.E., GOCAYNE J.D., UTTERBACK T.R., PETERSON J.D., KELLEY J.M.,
RA CORTON M.D., WEIDMAN J.M., FUJII C., BOWMAN C., WATREY L., MALLIN E.,
RA HAYES W.S., BORODOVSKIY M., KARP P.D., SMITH H.O., FRASER C.M.,
RA VENTER J.C.;
RT "The complete genome sequence of the gastric pathogen Helicobacter
RT pylori."
RL Nature 388:539-547(1997).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (PROBABLE).
CC -1- SIMILARITY: BELONGS TO THE DUF0077 (PECM) FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AE000628; AAO08277.1; -.
DR TIGR; HP1234; -.
CC -1- FUNCTION: DUF6; 1.
DR PFAM; PF00892; DUF6; 1.
KW Hypothetical protein; Transmembrane.
FT TRANSMEM 5 25
FT TRANSMEM 36 56
FT TRANSMEM 76 96
FT TRANSMEM 97 117
FT TRANSMEM 124 144
FT TRANSMEM 147 167
FT TRANSMEM 181 201
FT TRANSMEM 216 236
FT TRANSMEM 244 264
FT TRANSMEM 272 292
SQ SEQUENCE 298 AA; 32884 MW; A48B6A42 CRC32;

Query Match 47.7%; Score 74; DB 1; Length 298;
Best Local Similarity 41.2%; Pred. No. 4.19e-02;
Matches 7; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

Db 157 LSGTIVSLATITLDR 173
4 IAPVLEVTITLKKMR 20

RESULT 12
ID GBI_HELPY STANDARD; PRT; 353 AA.
AC P51876;
DI 01-OCT-1996 (Rel. 34, Created)
DI 01-OCT-1996 (Rel. 34, Last sequence update)
DI 15-DEC-1998 (Rel. 37, Last annotation update)
DE GUANINE NUCLEOTIDE-BINDING PROTEIN G(1), ALPHA SUBUNIT (ADENYLATE
DE CYCLASE-INHIBITING G ALPHA PROTEIN).

```

```

0S Helisoma trivolvis (Snail).
0C Eukaryota: Metazoa: Mollusca: Gastropoda: Pulmonata; Basommatophora;
0C Planorbidae; Helisoma.
0C
0C [1]
0C SEQUENCE FROM N.A.
0C
0C RC STRAIN-OREGON RED: TISSUE-CENTRAL GANGLION;
0C MEDLINE: 9418304.
0C
0C RA DUNGERMAN S., BAHLS F., RICHMOND J., DOYLE R.T., LARSON D.D.,
0C HAYDON P.G.;
0C "Roles for arachidonic acid and GTP-binding proteins in synaptic
0C transmission.";
0C RT J. Physiol. (Paris) 87:123-137(1993).
0C
0C RL J. FUNCTION: GUANINE NUCLEOTIDE-BINDING PROTEINS (G PROTEINS) ARE
0C INVOLVED AS MODULATORS OR TRANSDUCERS IN VARIOUS TRANSMEMBRANE
0C SIGNALING SYSTEMS.
0C
0C CC -1 SUBUNIT: G PROTEINS ARE COMPOSED OF 3 UNITS (ALPHA, BETA & GAMMA).
0C THE ALPHA CHAIN CONTAINS THE GUANINE NUCLEOTIDE BINDING SITE.
0C -1 SIMILARITY: BELONGS TO THE G-ALPHA FAMILY. SUBFAMILY 1
0C (G1/O/T/Z)).
0C
0C CC -----
0C CC This SWISS-PROT entry is copyright. It is produced through a collaboration
0C between the Swiss Institute of Bioinformatics and the EMBL outstation -
0C the European Bioinformatics Institute. There are no restrictions on its
0C use by non-profit institutions as long as its content is in no way
0C modified and this statement is not removed. Usage by and for commercial
0C entities requires a license agreement (see http://www.isb.ch/announce/
0C or send an email to license@isb-sib.ch).
0C
0C CC -----
0C DR EMBL: L18922; AAC41538.1; .
0C DR HSSP: P10824; IAS3.
0C DR PFW: PF00503; G-alpha: 1.
0C
0C KW GTP-binding; Transducer; ADP-ribosylation; Multigene family;
0C
0C KM
0C KW MYRISTATE.
0C
0C FT INT_MET 0 0 BY SIMILARITY.
0C FT LIPID 1 1 MYRISTATE (BY SIMILARITY).
0C FT NP_BIND 39 46 GTP (BY SIMILARITY).
0C FT NP_BIND 199 202 GTP (BY SIMILARITY).
0C FT NP_BIND 268 271 GTP (BY SIMILARITY).
0C FT MOD_RES 177 177 ADP-RIBOSYL[1] (BY ACTION OF CTX)
0C (BY SIMILARITY).
0C FT MOD_RES 350 350 ADP-RIBOSYL[1] (BY ACTION OF IAP)
0C (BY SIMILARITY).
0C
0C SQ SEQUENCE 353 AA: 40412 MW: 6680820 CRC32:
0C
0C Query Match 45.2%; Score 70; DB 1; Length 353;
0C Best Local Similarity 35.0%; Pred. No. 2,41e-01;
0C Matches 7; Conservative 8; Mismatches 5; Indels 0; Gaps 0;
0C
0C Db 294 TYEEAAAYIQLOFENLNKKK 313
0C
0C QY 1 TYEIAPEVLELYVTLKKMR 20
0C
0C RESULT 13
0C ID GBI_LTYMT STANDARD: PRT; 353 AA.
0C AC P30682;
0C
0C RC 01-APR-1993 (Rel. 25, Created)
0C DT 01-OCT-1994 (Rel. 30, Last sequence update)
0C DT 15-DEC-1998 (Rel. 37, Last annotation update)
0C DE GUANINE NUCLEOTIDE-BINDING PROTEIN G(I), ALPHA SUBUNIT (ADENYLATE
0C CYCLASE-INHIBITING G ALPHA PROTEIN).
0C OS Lymnaea stagnalis (great pond snail).
0C OC Eukaryota: Metazoa: Mollusca: Gastropoda: Pulmonata; Basommatophora;
0C Lymnaeidae: Lymnaea.
0C
0C RN [1]
0C RP SEQUENCE FROM N.A.
0C RC TISSUE-CNS;
0C RX MEDLINE: 93106153.
0C RA KNOL J.C., WEIDEMANN W., PLANTA R.J., VREUGDENHIL E.,
0C VAN HEEBRIKHUIZEN H.;
0C "Molecular cloning of G protein alpha subunits from the central
0C nervous system of the mollusc Lymnaea stagnalis.";
0C FLS Lett. 314:215-219(1992).

```

```
CC -1- FUNCTION: GAMINE NUCLEOTIDE-BINDING PROTEINS (G PROTEINS) ARE INVOLVED AS MODULATORS OR TRANSDUCERS IN VARIOUS TRANSMEMBRANE SIGNALING SYSTEMS.
CC CC
CC -1- FUNCTION: THE G(I) PROTEINS ARE INVOLVED IN HORMONAL REGULATION OF ADENYLATE CYCLASE; THEY INHIBIT THE CYCLASE IN RESPONSE TO BETA-ADRENERGIC STIMULI.
CC CC
CC -1- SUBUNIT: G PROTEINS ARE COMPOSED OF 3 UNITS (ALPHA, BETA & GAMMA). THE ALPHA CHAIN CONTAINS THE GUANINE NUCLEOTIDE BINDING SITE.
CC CC
CC -1- SIMILARITY: BELONGS TO THE G-ALPHA FAMILY. SUBFAMILY 1 (G(I/O/T/Z)).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
CC -----
DR EMBL, Z15095: CAA78807.1; -.
DR PIR, S25588; S25588.
DR PIR, S27013; S27013.
DR HSSP: P10824; IAS3.
DR PFAM: PF00503; G-alpha: 1.
KW GTP-binding; Transducer; ADP-ribosylation; Multigene family; Myristate.
KM
FT INIT_MET 0 0 BY SIMILARITY.
FT LIPID 1 1 MYRISTATE (BY SIMILARITY).
FT NP_BIND 39 46 GTP (BY SIMILARITY).
FT NP_BIND 199 202 GTP (BY SIMILARITY).
FT NP_BIND 268 271 GTP (BY SIMILARITY).
FT MOD_RES 177 177 ADP-RIBOSYL[1] (BY ACTION OF CTX) (BY SIMILARITY).
FT MOD_RES 350 350 ADP-RIBOSYL[1] (BY ACTION OF IAP) (BY SIMILARITY).
FT SEQUENCE 353 AA; 40355 MW; SCF27D61 CRC32;
SQ
Query Match . 45.2%; Score 70.; DB 1; Length 353;
Best Local Similarity 35.0%; Pred. No. 2,4le-01;
Matches 7; Conservative 8; Mismatches 5; Indels 0; Gaps 0;
Db 294 TYESAAAYIOLENTLKKK 313
Qy 1 TYELAFVLELYTLKMKR 20
RESULT 14
ID REGC_BACSU STANDARD: PRT: 682 AA.
AC Q34942;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DI 15-DEC-1998 (Rel. 37, Last annotation update)
DE ATP-DEPENDENT DNA HELICASE REGC (EC 3.6.1.-).
EC REGC.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Bacillus.
RN [1]
RP 'SEQUENCE FROM N.A.
RC STRAIN-168.
RA FOLUGER D., ERRINGTON J.;
RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
RC -1- FUNCTION: CRITICAL ROLE IN RECOMBINATION AND DNA REPAIR. HELP PROCESS HOLLADY JUNCTION INTERMEDIATES TO MATURE PRODUCTS BY CATALYSING BRANCH MIGRATION. HAS A DNA UNWINDING ACTIVITY CHARACTERISTIC OF A DNA HELICASE WITH A 3' TO 5' POLARITY. REGC UNWIND BRANCHED DUPLEX DNA (Y-DNA) (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE REGC SUBFAMILY OF HELICASES.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
```

```

CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL: Y13937; CAA74246.1; -
DR EMBL; 299112; CAB13460.1; -
DR SUBMITTER: BG13399; RECG.
DR PFAM: PF00270; DEAD; 1.
DR PFAM: PF00271; helicase_C.1.
KM Helicase; DNA repair; ATP-binding; DNA recombination; DNA-binding.
FT NP_BIND 284 291 ATP (POTENTIAL).
FT SITE 385 388 DEOH BOX.
SQ SEQUENCE 682 AA; 78140 MW; DEC00437 CRC32;
Db 141 IEPVYSKENVTKMMR 157
| 11: : | 11:11
4 IAPVFLVEYTLKKMR 20

Query Match 43.9%; Score 68; DB 1; Length 682;
Best Local Similarity 52.9%; Pred. No. 5,63e-01;
Matches 9; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

RESULT 15
ID DHS_C_BACSU STANDARD; PRT: 202 AA.
AC P08064.
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE SUCGINATE DEHYDROGENASE CYTOCHROME B-558 SUBUNIT.
GN SDHC.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Bacillus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-168 / PY79;
RX MEDLINE: 86223767.
RA MAGNUSON K., PHILIPS M.K., GUEST J.R., RUTBERG L.;
RT "Nucleotide sequence of the gene for cytochrome b558 of the Bacillus
RT subtilis succinate dehydrogenase complex.";
RL J. Bacteriol. 166:1067-1071(1986).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-168;
RX MEDLINE: 97124191.
RA WIPAT A., CARTER N., BRIGNELL C.S., GUY J.B., PIPER K.,
RA SANDERS J., EMERSON P.T., HARWOOD C.R.;
RT "The dnaB-phoA (256 degrees-240 degrees) region of the Bacillus
RT subtilis chromosome containing genes responsible for stress
RT responses, the utilization of plant cell walls and primary
RT metabolism.";
RL Microbiology 142:3067-3078(1996).
RN [3]
RP SEQUENCE OF 180-202 FROM N.A.
RC STRAIN-168 / PY79;
RX MEDLINE: 87109084.
RA PHILLIPS M.K., HEDERSTEDT L., HASNAIN S., RUTBERG L., GUEST J.R.;
RT "Nucleotide sequence encoding the flavoprotein and iron-sulfur
RT protein subunits of the Bacillus subtilis py79 succinate
RT dehydrogenase complex.";
RL J. Bacteriol. 169:864-873(1987).
RN [4]
RP SEQUENCE OF 1-13 FROM N.A.
RX MEDLINE: 87250294.
RA MELIN L., MAGNUSON K., RUTBERG L.;
RT "Identification of the promoter of the Bacillus subtilis sdh operon.";
RL J. Bacteriol. 169:3232-3236(1987).
RN [5]
RP TOPOLOGY, AND HEME-BINDING.
RX MEDLINE: 91014684.
RA FRIDEN H., HEDERSTEDT L.;
RT "Role of His residues in Bacillus subtilis cytochrome b558 for haem

```

```

binding and assembly of succinate: quinone oxidoreductase (complex
II).".
RL Mol. Microbiol. 4:1045-1056(1990).
CC -1- FUNCTION: DI-HEME CYTOCHROME OF THE SUCCINATE DEHYDROGENASE
CC COMPLEX. THE MID-POINT REDOX POTENTIAL IS +65mV.
CC -1- PATHWAY: TRICARBOXYLIC ACID CYCLE.
CC -1- SUBUNIT: PART OF AN ENZYME COMPLEX CONTAINING THREE SUBUNITS:
CC A FLAVOPROTEIN, AN IRON-SULFUR PROTEIN AND CYTOCHROME B-558.
CC -1- SIMILARITY: TO CYTOCHROME B FROM W. SUCCINOGENES FUMARATE
CC REDUCTASE.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M13470; AAA23745.1; -
DR EMBL; Z75208; CAA99546.1; -
DR EMBL; M16753; AAA22749.1; -
DR EMBL; Z99118; CAB14805.1; -
DR PIR; A29843; DEBSSC.
DR SUBTILIST; BG10351; SDHC.
KW Tricarboxylic acid cycle; Transmembrane; Electron transport; Heme.
FT TRANSMEM 12 31 POTENTIAL.
FT TRANSMEM 60 79 POTENTIAL.
FT TRANSMEM 93 113 POTENTIAL.
FT TRANSMEM 135 155 POTENTIAL.
FT TRANSMEM 178 196 POTENTIAL.
FT BINDING 28 28 HEME (PROBABLE).
FT BINDING 70 70 HEME (PROBABLE).
FT BINDING 113 113 HEME (POTENTIAL).
FT BINDING 155 155 HEME (PROBABLE).
SQ SEQUENCE 202 AA; 22931 MW; AA2D4162 CRC32;

Query Match 43.2%; Score 67; DB 1; Length 202;
Best Local Similarity 52.9%; Pred. No. 8,56e-01;
Matches 9; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

Db 180 TYVTLLIFVALSYGLK 196
Oy 1 TYETAPVFLLEIVTLK 17

Search completed: Tue Mar 7 21:50:10 2000
Job time : 6 secs.

```





```

DT 01-NOV-1999 (TREMblrel. 12, Last annotation update)
DE 67MD GLUTAMIC ACID DECARBOXYLASE.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
RN Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RP [1]
RC SEQUENCE FROM N.A.
RA STRAIN-BALB/C.
RA AUST G., STEINBRENNER H., THAMM B., ROST A.K., SEISSELER J.,
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
CC -I- COPACATOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).
CC -I- SIMILARITY: BELONGS TO GROUP II DECARBOXYLASES (DDC, GAD, HDC AND
CC TYRDC).
DR EMBL: Y12257; GAN72934.1; -.
DR PROSITE: PS00392; DDC_GAD_HDC_YDC; 1.
DR PFM: PF00282; pyridoxal_dec; 1.
KW Lyase; Decarboxylase; Pyridoxal phosphate.
SQ SEQUENCE 593 AA; 66648 MW; BAFE92E0 CRC32;

Query Match
Best Local Similarity 84.5%; Score 131; DB 11; Length 593;
Matches 17; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 214 TTEIAPVFLLEYVTLKKMR 233
OY 1 TTEIAPVFLLEYVTLKKMR 20

RESULT 3
ID 09W656 PRELIMINARY; PRT; 182 AA.
AC 09W656.
DT 01-NOV-1999 (TREMblrel. 12, Created)
DT 01-NOV-1999 (TREMblrel. 12, Last sequence update)
DT 01-NOV-1999 (TREMblrel. 12, Last annotation update)
DE GLUTAMATE DECARBOXYLASE ISOFORM 65 (EC 4.1.1.15) (FRAGMENT).
GN GAD65.
OS Coryphaenoides armatus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
OC Neopterygii; Teleostei; Euteleostei; Paracanthopterygii; Gadiformes;
OC Macrouridae; Coryphaenoides.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RX MEDLINE: 99261650.
RA BOSMA P.T., BLAZQUEZ M., COLLINS M.A., BISHOP J.D.D., DROUIN G.,
RA PRIEDE I.G., DOCHERTY K., TRUDEAU V.L.;
RT "Multiplicity of glutamic acid decarboxylases (GAD) in vertebrates:
RT molecular phylogeny and evidence for a new GAD paralog.";
RL Mol. Biol. Evol. 16:397-404(1999).
DR EMBL: AF043267; AAD22713.1; -.
KW Lyase.
FT NON_TER
SQ SEQUENCE 182 AA; 182 MW; 1225481D CRC32;

Query Match
Best Local Similarity 83.9%; Score 130; DB 13; Length 182;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 1 VAPFVLLLEYVTLKKMR 17
OY 4 IAPFVLLLEYVTLKKMR 20

RESULT 4
ID 09W654 PRELIMINARY; PRT; 182 AA.
AC 09W654.
DT 01-NOV-1999 (TREMblrel. 12, Created)
DT 01-NOV-1999 (TREMblrel. 12, Last sequence update)
DT 01-NOV-1999 (TREMblrel. 12, Last annotation update)
DE GLUTAMATE DECARBOXYLASE ISOFORM 65 (EC 4.1.1.15) (FRAGMENT).
GN GAD65.
OC Carassius auratus (Goldfish).

```

```

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
OC Neopterygii; Teleostei; Euteleostei; Ostariophysi; Cypriniformes;
OC Cyprinoidae; Cyprinidae; Cyprininae; Carassius.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RX MEDLINE: 99261650.
RA BOSMA P.T., BLAZQUEZ M., COLLINS M.A., BISHOP J.D.D., DROUIN G.,
RA PRIEDE I.G., DOCHERTY K., TRUDEAU V.L.;
RT "Multiplicity of glutamic acid decarboxylases (GAD) in vertebrates:
RT molecular phylogeny and evidence for a new GAD paralog.";
RL Mol. Biol. Evol. 16:397-404(1999).
DR EMBL: AF043265; AAD22711.1; -.
KW Lyase.
FT NON_TER
SQ SEQUENCE 182 AA; 20097 MW; AAA23079 CRC32;

Query Match
Best Local Similarity 83.9%; Score 130; DB 13; Length 182;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 1 VAPFVLLLEYVTLKKMR 17
OY 4 IAPFVLLLEYVTLKKMR 20

RESULT 5
ID 09W662 PRELIMINARY; PRT; 56 AA.
AC 09W662.
DT 01-NOV-1999 (TREMblrel. 12, Created)
DT 01-NOV-1999 (TREMblrel. 12, Last sequence update)
DT 01-NOV-1999 (TREMblrel. 12, Last annotation update)
DE GLUTAMATE DECARBOXYLASE ISOFORM 65 (EC 4.1.1.15) (FRAGMENT).
GN GAD65.
OS Pseudemys scripta (Slider turtle).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Testudines;
OC Cryptodira; Testudinoidea; Emydidae; Trachemys.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RX MEDLINE: 99261650.
RA BOSMA P.T., BLAZQUEZ M., COLLINS M.A., BISHOP J.D.D., DROUIN G.,
RA PRIEDE I.G., DOCHERTY K., TRUDEAU V.L.;
RT "Multiplicity of glutamic acid decarboxylases (GAD) in vertebrates:
RT molecular phylogeny and evidence for a new GAD paralog.";
RL Mol. Biol. Evol. 16:397-404(1999).
DR EMBL: AF043273; AAD22719.1; -.
KW Lyase.
FT NON_TER
SQ SEQUENCE 56 AA; 6236 MW; 6CEAA826 CRC32;

Query Match
Best Local Similarity 94.1%; Pred. No. 3.22e-12;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 1 IAPFVLLLEYVTLKKMR 17
OY 4 IAPFVLLLEYVTLKKMR 20

RESULT 6
ID 09W661 PRELIMINARY; PRT; 182 AA.
AC 09W661.
DT 01-NOV-1999 (TREMblrel. 12, Created)
DT 01-NOV-1999 (TREMblrel. 12, Last sequence update)
DT 01-NOV-1999 (TREMblrel. 12, Last annotation update)
DE GLUTAMATE DECARBOXYLASE ISOFORM 65 (EC 4.1.1.15) (FRAGMENT).
GN GAD65.
OS Pseudemys scripta (Slider turtle).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Testudines;
OC Cryptodira; Testudinoidea; Emydidae; Trachemys.
RN [1]

```

```

RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN.
RX MEDLINE; 99261650.
RA BOSMA P.T., BLAQUEZ M., COLLINS M.A., BISHOP J.D.D., DROUIN G.,
RI PRIEDE I.G., DOCHERRY K., TRUDEAU V.L.;
RT "Multiplicity of glutamic acid decarboxylases (GAD) in vertebrates:
  Molecular phylogeny and evidence for a new GAD paralog."
RL Mol. Biol. Evol. 16:397-404(1999).
RN EMBL; AF043272; AAD22718.1; -.
KW Lyase.
FT NON_TER
SQ SEQUENCE 182 AA; 19942 MW; 1699125D CRC32;

Query Match
Best Local Similarity 94.1%; Score 129; DB 13; Length 182;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 1 IAPVFLLEYVTLKMR 17
   |||||
OY 4 IAPVFLLEYVTLKMR 20

RESULT 7
ID 09W659 PRELIMINARY; PRT: 182 AA.
AC 09W659;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
DE GLUTAMATE DECARBOXYLASE ISOFORM 65 (EC 4.1.1.15) (FRAGMENT).
GN GAD65
OS Poephila guttata (zebra finch) (Taeniopygia guttata).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Aves;
OC Neognathae; Passeriformes; Estrildidae; Estrildinae; Taeniopygia.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN.
RX MEDLINE; 99261650.
RA BOSMA P.T., BLAQUEZ M., COLLINS M.A., BISHOP J.D.D., DROUIN G.,
RI PRIEDE I.G., DOCHERRY K., TRUDEAU V.L.;
RT "Multiplicity of glutamic acid decarboxylases (GAD) in vertebrates:
  Molecular phylogeny and evidence for a new GAD paralog."
RL Mol. Biol. Evol. 16:397-404(1999).
RN EMBL; AF043270; AAD22716.1; -.
KW Lyase.
FT NON_TER
SQ SEQUENCE 182 AA; 19918 MW; B67EADF CRC32;

Query Match
Best Local Similarity 94.1%; Score 129; DB 13; Length 182;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 1 IAPVFLLEYVTLKMR 17
   |||||
OY 4 IAPVFLLEYVTLKMR 20

RESULT 8
ID 09Y158 PRELIMINARY; PRT: 590 AA.
AC 09Y158;
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
DE GLUTAMATE DECARBOXYLASE 67.
GN GAD67.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;
OC Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-WHITE LECHORN;
RA WAGBERG F.;

```

```

RT "Characterization of glutamate decarboxylase in chicken."
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
CC -1- COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO GROUP II DECARBOXYLASES (DDC, GAD, HDC AND
  TYRDC).
DR EMBL; AF030355; AAD01902.1; -.
DR PROSITE; PS00392; DDC_GAD_HDC_YDC; 1.
KW Lyase; Decarboxylase; Pyridoxal phosphate.
SQ SEQUENCE 590 AA; 66710 MW; 80B66DFF CRC32;

Query Match
Best Local Similarity 80.0%; Score 128; DB 13; Length 590;
Matches 16; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db 211 TYETAPVFLMEQTLKMR 230
   |||||
OY 1 TYETAPVFLMEQTLKMR 20

RESULT 9
ID 09J276 PRELIMINARY; PRT: 232 AA.
AC 09J276;
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
DE GLUTAMATE DECARBOXYLASE (EC 4.1.1.15) (FRAGMENT).
GN GAD67.
OS Brachydanio rerio (zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
OC Neopterygii; Teleostei; Euteleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Cyprinidae; Rasbora; Danio.
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE; 98295903.
RA MARTIN S.C., HEINRICH G., SANDELL J.H.;
RT "Sequence and expression of glutamic acid decarboxylase isoforms in
  the developing zebrafish."
RL J. Comp. Neurol. 396:253-266(1998).
CC -1- COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO GROUP II DECARBOXYLASES (DDC, GAD, HDC AND
  TYRDC).
DR EMBL; AF017266; AAC24327.1; -.
DR PROSITE; PS00392; DDC_GAD_HDC_YDC; 1.
DR PFM; PF00282; pyridoxal_dec; 1.
KW Lyase; Decarboxylase; Pyridoxal phosphate.
FT NON_TER
SQ SEQUENCE 232 AA; 25676 MW; C7DC7A63 CRC32;

Query Match
Best Local Similarity 85.0%; Score 127; DB 13; Length 232;
Matches 17; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 2 TYETAPVFLMEQTLKMR 21
   |||||
OY 1 TYETAPVFLMEQTLKMR 20

RESULT 10
ID 09I644 PRELIMINARY; PRT: 563 AA.
AC 09I644;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
DE GLUTAMIC ACID DECARBOXYLASE.
GN GAD.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Amphibia;
OC Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae; Xenopodinae;
OC Xenopus.
RN [1]
RP SEQUENCE FROM N.A.
RA WATT S.D., SPITZER N.C.;

```

```

RL Submitted (OCT-1995) to the EMBL/Genbank/DBI databases.
CC -i- COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).
CC -i- SIMILARITY: BELONGS TO GROUP II DECARBOXYLASES (DDC, GAD, HDC AND TYRDC).
CC DR EMBL: U38225; AAA96273.1; -.
CC DR PROSITE: PS00392; DDC_GAD_HDC_YDC; 1.
CC DR PFAM: PF00282; pyridoxal_dec; 1.
CC DR Lyase; Decarboxylase; Pyridoxal phosphate.
CC SQ SEQUENCE 563 AA; 64095 MW; CBB0C98 CRC32;

Query Match
Best Local Similarity 78.9%; Score 123; DB 13; Length 563;
Matches 15; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db 185 TTEIAPFVLEMETVTLTKMR 203
QY 2 TTEIAPFVLEMETVTLTKMR 20
|||||:|:|:|:|

RESULT 11
ID 044102 PRELIMINARY; PRT; 370 AA.
AC 044102;
DT 01-JUN-1998 (TREMBlrel. 06, Created)
DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
DE GLUTAMIC ACID DECARBOXYLASE (FRAGMENT).
DE GN GAD1.
OS Drosophila pseudobscura (Fruit fly).
CC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
CC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
CC Ephydroidea; Drosophilidae; Drosophila.
RN [1]
RP SEQUENCE FROM N.A.
RA ZENG L.-W., COMERON J.M., CHEN B., KREITMAN M.;
RL Genetic 0:0-0(1997).
DR EMBL: AF025807; AAB87892.1; -.
DR HSSP: P06543; 100D.
DR FLIBASE: FBgn0023295; DpseGad1.
DR PFAM: PF00282; pyridoxal_dec; 2.
FT NON_TER 1
FT SEQUENCE 370 AA; 41887 MW; A1EB456F CRC32;

Query Match
Best Local Similarity 78.1%; Score 121; DB 5; Length 370;
Matches 15; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Db 52 TTEIAPFVLEMETVTLTKMR 71
QY 1 TTEIAPFVLEMETVTLTKMR 20
|||||:|:|:|:|

RESULT 12
ID 044103 PRELIMINARY; PRT; 370 AA.
AC 044103;
DT 01-JUN-1998 (TREMBlrel. 06, Created)
DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
DE GLUTAMIC ACID DECARBOXYLASE (FRAGMENT).
DE GN GAD1.
OS Drosophila subobscura (Fruit fly).
CC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
CC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
CC Ephydroidea; Drosophilidae; Drosophila.
RN [1]
RP SEQUENCE FROM N.A.
RA ZENG L.-W., COMERON J.M., CHEN B., KREITMAN M.;
RL Genetic 0:0-0(1997).
DR EMBL: AF025808; AAB87893.1; -.
DR HSSP: P06543; 100C.
DR FLIBASE: FBgn0023244; DsubGad1.
DR PFAM: PF00282; pyridoxal_dec; 2.
FT NON_TER 1
FT SEQUENCE 370 AA; 41887 MW; A1EB456F CRC32;

```

```

FT NON_TER 370 370
SQ SEQUENCE 370 AA; 41923 MW; D75BDC49 CRC32;

Query Match
Best Local Similarity 78.1%; Score 121; DB 5; Length 370;
Matches 15; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Db 52 TTEIAPFVLEMETVTLTKMR 71
QY 1 TTEIAPFVLEMETVTLTKMR 20
|||||:|:|:|:|

RESULT 13
ID 064577 PRELIMINARY; PRT; 478 AA.
AC 064577;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
DE CYSTEINE SULFINIC ACID DECARBOXYLASE (EC 4.1.1.29)
DE (SULFINOALANINE DECARBOXYLASE) (CYSTEINE-SULFINATE DECARBOXYLASE).
OS Rattus norvegicus (Rat).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
CC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN-SPRAGUE-DAWLEY;
RL MEDLINE: 95290499.
RA KAIKAKIA P.J., JERKINS A.A., GOODSPED D.C., STEELE R.D.;
RT "Cloning and characterization of rat cysteine sulfinate acid
  decarboxylase."
RL Biochim. Biophys. Acta 1262:79-82(1995).
CC -i- CATALYTIC ACTIVITY: 3-SULFINO-L-ALANINE = HYPOTAURINE + CO(2).
CC -i- COFACTOR: PYRIDOXAL-PHOSPHATE.
CC -i- SIMILARITY: BELONGS TO GROUP II DECARBOXYLASES (DDC, GAD, HDC AND TYRDC).
CC DR EMBL: M64755; AAC42063.1; -.
CC DR PROSITE: PS00392; DDC_GAD_HDC_YDC; 1.
CC DR PFAM: PF00282; pyridoxal_dec; 1.
CC DR Lyase; Decarboxylase; Pyridoxal phosphate.
CC SQ SEQUENCE 478 AA; 53725 MW; 4CAC0093 CRC32;

Query Match
Best Local Similarity 71.6%; Score 111; DB 11; Length 478;
Matches 15; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Db 117 TTEIAPFVLEMETVTLTKMR 136
QY 1 TTEIAPFVLEMETVTLTKMR 20
|||||:|:|:|:|

RESULT 14
ID 064611 PRELIMINARY; PRT; 493 AA.
AC 064611;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
DE CYSTEINE SULFINATE DECARBOXYLASE (EC 4.1.1.29)
DE (SULFINOALANINE DECARBOXYLASE) (CYSTEINE-SULFINATE DECARBOXYLASE).
DE GN CSD.
OS Rattus norvegicus (Rat).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
CC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE: 96283809.
RA REYMOND I., SERGEANT A., TAPPAZ M.;
RT "Molecular cloning and sequence analysis of the cDNA encoding rat
  liver cysteine sulfinate decarboxylase (CSD).";
RL Biochim. Biophys. Acta 1307:152-156(1996).
CC -i- COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).
CC -i- SIMILARITY: BELONGS TO GROUP II DECARBOXYLASES (DDC, GAD, HDC AND TYRDC).

```

DR EMBL: X94152; CAA63868.1; -  
 DR PROSITE: PS00392; DDC\_GAD\_HDC\_YDC; 1.  
 DR PRAM: PF00282; Pyridoxal\_dec; 1.  
 KW lyase: decarboxylase; Pyridoxal phosphate.  
 SQ SEQUENCE 493 AA; 55248 MW; D7A6D9A CRC32;

Query Match 71.6%; Score 111; DB 11; Length 493;  
 Best Local Similarity 75.0%; Pred. No. 2.11e-08;  
 Matches 15; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

DB 117 TYEIAPVFLMEEEVLKLR 136  
 |||||  
 QY 1 TYEIAPVFLLEVYTLKKMR 20

RESULT 15  
 ID 09Y602 PRELIMINARY; PRT; 267 AA.  
 AC 09Y602;  
 DT 01-NOV-1999 (TREMBlrel. 12, Created)  
 DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)  
 DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)  
 DE CYSTEINE SULFINIC ACID DECARBOXYLASE-RELATED PROTEIN 1.  
 GN CSAD.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 OC Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 RN [1]  
 RP SEQUENCE FROM N. A.  
 RC TISSUE-BRAIN;  
 RA PRITCHARD J.E., RAMSDEN D.B.;  
 RT "Human cysteine sulfinic acid decarboxylase (CSAD)-related mRNA, 1.";  
 RL Submitted (DEC-1998) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: AF16545; AAD32543.1;  
 SQ SEQUENCE 267 AA; 30264 MW; A3475A7D CRC32;

Query Match 69.7%; Score 108; DB 4; Length 267;  
 Best Local Similarity 70.0%; Pred. No. 8.76e-08;  
 Matches 14; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

DB 117 TYEIAPVFLMEEEVLKLR 136  
 |||||  
 QY 1 TYEIAPVFLLEVYTLKKMR 20

Search completed: Tue Mar 7 21:52:06 2000  
 Job time : 13 secs.

THIS PAGE BLANK (USPTO)